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**GenCore version 5.1.7**  
**Copyright (c) 1993 - 2006 Biocceleration Ltd.**  
**M protein - protein search, using sw model**  
**run on: March 1, 2006, 02:42:12 ; Search time 81 Seconds**  
**(without alignments)**  
**48.820 Million cell updates/sec**  
**title: US-09-583-200F-22**  
**perfect score: 41**  
**sequence: I RLIQETLV 9**  
**coring table: BLOSUM62**  
**Gapop 10.0 , Gapext 0.5**  
**searched: 2443163 seqs, 439378781 residues**  
**total number of hits satisfying chosen parameters: 2443163**

## ALIGNMENTS

obt-processing: Minimum Match 0% Max match 100%

Listing first 45 summaries

database : A\_Geneseq\_21:  
1: geneset100001:

geneseqpt9906: \* 22

geneseqP20016: \* 4: 5:

genesept 2003a: 6-7

genetische 2005; 48: 88-94

No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed.

SUMMARIES

result	No.	Query Score	Match Length	DB ID	Description	
1	41	100.0	9	AAR59123	Peptide f	
	2	41	100.0	9	AAW36829	ImmunoGen
	3	41	100.0	9	ARN70055	Herr-2/neu
	4	41	100.0	9	AAB99701	HLA A2 bi
	5	41	100.0	9	AAGB8770	HERR2/neu
	6	41	100.0	9	AAGB93002	HERR2/neu
	7	41	100.0	9	ABG79079	Human HER
	8	41	100.0	9	AAE26825	Human HER
	9	41	100.0	9	AEE31139	Human erb
	10	41	100.0	9	AEA36131	Human BGF
	11	41	100.0	9	ADA49636	Multi -epi
	12	41	100.0	9	ABD02798	Cytotoxic
	13	41	100.0	9	ABW00310	HBR-2 HLA
	14	41	100.0	9	ADEP97585	ImmunoGen
	15	41	100.0	9	ADGB8645	Class I H
	16	41	100.0	9	ADM1641	MHC class
	17	41	100.0	9	ADM16395	MHC class
	18	41	100.0	9	ADQ24294	Unidentif
	19	41	100.0	9	ADO38874	Human Her
	20	41	100.0	9	ADP79772	Human HLA
	21	41	100.0	9	ADU04945	HPR-2/neu
	22	41	100.0	9	ADU66573	Cancer -ab
	23	41	100.0	9	ADW88104	Human T
	24	41	100.0	9	ADY00595	Class I H

W032401Z - ALL.  
15-SEP-1994.

Example 5; Page 100; 138PP; 1  
 AAR59104-264 are immunogenic  
 binding motif. These peptides  
 of at least 15 as compared to  
 has an IC50 of 0.091 and the  
 ERBB Proteins. The peptides o  
 lymphocytes which can react

CC treatment or prophylaxis of cancer, e.g. prostate cancer or lymphoma, etc.  
 CC (Updated on 25-MAR-2003 to correct PN field.)

XX SQ Sequence 9 AA;

Query Match 100.0%; Score 41; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2e+06; Mismatches 0; Indels 0; Gaps 0;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLLQETELV 9  
 YY 1 RLLQETELV 9  
 Db 1 RLLQETELV 9

RESULT 3  
 AAW70055  
 ID AAW70055 standard; peptide; 9 AA.

XX AAW70055;  
 ID AAW70055;  
 AC AAW70055;  
 DT 22-OCT-1998 (first entry)  
 XX HER-2/neu derived HLA-A2.1 binding peptide 3 (residues 689-697).

XX Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;  
 KW human leukocyte antigen; HLA; tumour associated antigen; cancer;  
 KW antigen presenting cell; APC; immunogenic peptide; immune disorder;  
 KW viral infection; AIDS; hepatitis; bacterial infection; malaria;  
 KW fungal infection; tuberculosis; melanoma; HER-2/neu; cerB-2.

OS Synthetic.  
 OS Homo sapiens.  
 PN W09732603-A1.  
 XX PD 12-SEP-1997.  
 XX PF 05-MAR-1997; 97WO-US003611.  
 XX PR 05-MAR-1996; 96US-0012845P.  
 XX PA (SCRI ) SCRIPPS RES INST.  
 XX PI Sherman LA, Lustgarten J;  
 XX DR 1997-470496/43.  
 XX PR Nucleic acid encoding variable regions of HLA-restricted non-human T cell receptor specific for tumour antigen - used to identify tumour antigens and for tumour therapy.

Example 1: Page 9; 34pp; English.

XX PS Synthetic peptides AAM26824-40 are based on the sequence of the human Her neu protein, wherein each sequence contains the anchor motif for human leukocyte antigen (HLA) A2.1. The present peptide is based on positions 689-697. The ability of these peptides to inhibit the binding of an influenza virus matrix protein peptide M1 to HLA A2.1 was measured by inhibition of lysis by an M1 specific, cytotoxic T lymphocyte (CTL) clone. The present protein showed 56% inhibition. The peptides were also tested for their ability to elicit an immune response in vivo. However, only H3 (AAW36824) and H7 (AAW36826) were able to do this. H3 and H7 peptides are tumour-associated antigens, and were used to immunize a transgenic, non-human vertebrate (that has been modified to express at least one HLA antigen), so that the animal produces CTL which displays HLA-restricted T-cell receptor (TCR) specificity for the antigen. Nucleic acid encoding variable regions of the alpha and beta chains of such TCRs can be amplified from CTLs produced in the above manner. Cells expressing recombinant TCR are used to identify antigens associated with a tumour and to treat tumours in humans. Transgenic mice are a more convenient source of CTL than the tumour-infiltrating lymphocytes previously used. TCR can be humanised to reduce side-reactions and short peptide derivatives of TCR are more economical to produce than TCR itself, particularly when expressed as a single-chain molecule rather than as a dimer.

XX SQ Sequence 9 AA;

Query Match 100.0%; Score 41; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2e+06; Mismatches 0; Indels 0; Gaps 0;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLLQETELV 9  
 Db 1 RLLQETELV 9

RESULT 3  
 AAW70055  
 ID AAW70055 standard; peptide; 9 AA.

XX AAW70055;  
 AC AAW70055;  
 DT 22-OCT-1998 (first entry)  
 XX HER-2/neu derived HLA-A2.1 binding peptide 3 (residues 689-697).

XX Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;  
 KW human leukocyte antigen; HLA; tumour associated antigen; cancer;  
 KW antigen presenting cell; APC; immunogenic peptide; immune disorder;  
 KW viral infection; AIDS; hepatitis; bacterial infection; malaria;  
 KW fungal infection; tuberculosis; melanoma; HER-2/neu; cerB-2.

OS Synthetic.  
 OS Homo sapiens.  
 PN W09833888-A1.  
 XX PD 06-AUG-1998.  
 XX PF 30-JAN-1998; 98WO-US001959.  
 XX PR 31-JAN-1997; 97US-0036696P.  
 XX PA (EPIM-) EPIMMUNE INC.

Production of antigen-specific cytotoxic T cells - by incubating peptide(s) from antigen that binds class I major histocompatibility complex molecules with pre-treated antigen presenting cells.

Example 7: Page 77; 104pp; English.

XX Sequences shown in AAW70053 to AAW70075 represent peptides derived from HER-2/neu (cerB-2) antigen. The peptides can bind to a human leukocyte antigen (HLA) HLA-A2.1 and are used to exemplify the method of invention of producing antigen-specific cytotoxic T cells (CTLs) in vitro. The method comprises contacting immunogenic peptides from an antigen that binds class I major histocompatibility complex (MHC) molecules with antigen presenting cells (APCs) prereated with pretreatment growth factors, and incubating the APCs with purified CD8 cells in the presence of at least 2 incubation growth factors, thereby producing antigen-specific CTLs. A method for specifically killing target cells in a human patient is also provided which comprises obtaining a fluid sample containing CTLs from a patient, contacting the cytotoxic T cells with APCs prereated with pre-treatment growth factors, where the APCs comprise class I MHC molecules. The prereated APCs are incubated with the cytotoxic growth factors, thereby producing activated CTLs which are contacted with a carrier to form a composition. The composition can then be administered to the patient. The activated CTLs can be used for treating cancers, immune disorders, viral infections, AIDS, hepatitis, bacterial infection, fungal infection, malaria or tuberculosis.

Sequence 9 AA;





CC the cancer treatment. The present sequence is a tumour antigen derived  
CC epitope for inclusion in the composition of the invention

SQ Sequence 9 AA;

Query Match Score 41; DB 5; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX Human; T-lymphocyte; vaccine; viral infection; gene therapy; cancer.

QY 1 RLLQETELV 9

Db 1 RLLQETELV 9

RESULT 8

ID AAB26825 standard; peptide; 9 AA.

XX AAB26825;

XX DT 13-DEC-2002 (first entry)

XX PR 29-AUG-2002.

XX PD 19-FEB-2002.

XX PF 19-FEB-2002; 2002WO-US005748.

XX PR 20-FEB-2001; 2001US-0270252P.

XX PA (ORTH ) ORTHO-MCNELL PHARM INC.

XX XX

XX PI Debray J, Moriarty A, Leturcq DJ, Jackson MR, Peterson PA;

XX PI Heiskala M;

XX DR WPI; 2002-667033/71.

XX PS Example 3; Page 98; 99PP; English.

XX SQ Sequence 9 AA;

Query Match Score 41; DB 5; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX Human; T-lymphocyte; vaccine; viral infection; gene therapy; cancer.

QY 1 RLLQETELV 9

Db 1 RLLQETELV 9

CC Treating a subject with cancer comprises combining the CD4+ cells, which  
PR are stimulated with non-naturally occurring antigen-presenting cell line,  
PR with adherent blood monocytes and inoculating the subject with CD8+  
PR suspension.  
XX PS Example 3; Page 98; 99PP; English.

CC The invention relates to a method of treating a subject with cancer. The  
CC method involves combining the CD4+ cells, which are stimulated with non  
CC naturally occurring antigen-presenting cell (mAPC) line, with adherent  
CC blood monocytes and inoculating the subject with CD8+ suspension. The  
CC method is useful for treating cancer e.g. ovarian cancer, breast cancer  
CC and melanoma etc. It is also useful in cell therapy. The present sequence  
CC is human HER-2/neu peptide used to illustrate method of the invention

SQ Sequence 9 AA;

Query Match Score 41; DB 5; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2e+06;

XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX Human; T-lymphocyte; vaccine; viral infection; gene therapy; cancer.

QY 1 RLLQETELV 9

Db 1 RLLQETELV 9

RESULT 9

ID AAB31139 standard; peptide; 9 AA.

XX DT 02-JUN-2005.

CC the cancer treatment. The present sequence is a tumour antigen derived  
CC epitope for inclusion in the composition of the invention

SQ Sequence 9 AA;

Query Match Score 41; DB 5; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2e+06;

XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX Human; T-lymphocyte; vaccine; viral infection; gene therapy; cancer.

QY 1 RLLQETELV 9

Db 1 RLLQETELV 9

RESULT 10

ID AAB36331 standard; peptide; 9 AA.

XX AC AAB36331;

XX DT 11-AUG-2005 (first entry)

XX PR Human EGFR cytotoxic T-lymphocyte epitope Peptide - SEQ ID 41.

XX KW viral infection; viricide; cytostatic; tumor; neoplasm; cell therapy;

XX KW antigen; Endothelial growth factor receptor; EGFR.

XX OS Homo sapiens.

XX PN JP2005139118-A.

XX DR 02-JUN-2005.

XX	07-NOV-2003; 2003JP-00377653.	PA (BROW/) BROWN D H.
PF		XX Sette A, Chesnut R, Livingston BD, Baker DM, Newman MJ, Brown DH;
PR	20-FEB-2001; 2001US-0270252P.	XX PI
XX		XX DR WPI; 2003-615704/58.
PA	(ORTHO ) ORTHO-MCNEIL PHARM INC.	XX PT Designing multi-epitope construct having major histocompatibility complex class I and II epitope nucleic acids, by selecting mixture of amino acid insertions at junctions of construct to minimize junctional epitopes.
XX	Leturco DJ, Moriarty AM, Jackson MR, Peterson PA, Richards JM;	XX PR Disclosure; Fig 19D; 78pp; English.
PI		XX
XX	PWI; 2002-667033/71.	The invention relates to a method of designing multi-epitope constructs comprising major histocompatibility complex (MHC) class I and II (CTL) epitope nucleic acids (CEN), introducing CEN, introducing flanking amino acid residue selected from specified amino acid residues given in specification at C+1 position of CEN, introducing amino acid spacer residues between two CEN, and selecting the constructs having less junctional epitopes. The method is useful for designing multi-epitope construct having multiple epitope nucleic acid. The method avoids or minimises the occurrence of junctional epitopes and maximises the immunogenicity and/or antigenicity of multi-epitope vaccines. The present sequence represents the amino acid sequence of an epitope present in a multi-epitope construct.
PT	Treating a subject with cancer comprises combining the CD8+ cells, which are stimulated with non-naturally occurring antigen-presenting cell line, with adherent blood monocytes and inoculating the subject with CD8+ cell suspension.	XX PS Example 3; SEQ ID NO 41; 65pp; Japanese.
XX		XX
CC	The invention relates to a novel method for treating viral infection in a subject. The method comprises preparing an antigen presentation cell lineage (mAPC), collecting CD8+ cells from the subject, stimulating CD8+ cells using the mAPC, culturing the CD8+ cells in the presence of interleukin-2 (IL-2) and/or IL-7, mixing peripheral blood monocytes from the subject, subjecting the components to gamma irradiation, combining the CD8+ cells with adhesive peripheral blood monocytes and inoculating the CD8+ suspended solid to the subject. The method of the invention demonstrates virucide and cytosolic activities and may be useful for treating a viral infection or tumor in a subject via cell therapy. The current sequence is that of a human EGFR cytotoxic T-lymphocyte peptide of the invention which was incorporated into a Drosophila antigen presenting cell.	XX PS
CC		XX SQ Sequence 9 AA;
CC		XX Query Match Score 41; DB 5; Length 9;
CC		XX Best Local Similarity 100.0%; Prod. No. 2e+06; Mismatches 0; Indels 0; Gaps 0;
CC		XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC		XX Qy 1 RLLQETELY 9
CC		XX Db 1 RLLQETELY 9
CC		RESULT 12
CC		ID ABC007298 Standard: Peptide: 9 AA.
DE		XX Cytotoxic T-lymphocyte (CTL)-stimulating peptide #26.
XX		XX Human; HER-2/neu proto-oncogene; HER-2; cytotoxic T-lymphocyte; CTL;
AC		XX CTL-stimulating peptide; immune response; breast cancer;
XX		XX proliferative disorder; ovarian cancer; anti-cancer vaccine;
DT		XX molecular weight standard; chromatographic column; cytostatic.
XX		XX Homo sapiens.
DE		XX Synthetic.
XX		XX PN US6514942-B1.
XX		XX PA (TEXA ) UNIV TEXAS SYSTEM.
OS		XX PD 04-FEB-2003.
DB		XX PF 14-MAR-1995; 95US-00403459.
XX		XX PR 14-MAR-1995; 95US-00403459.
AC		XX DT 20-NOV-2003 (first entry)
ADA49636		XX Multi-epitope construct specific peptide #178.
ADA49636		XX Multi-epitope; immunogenic; epitope; major histocompatibility complex; MHC class I; MHC class II; junctional epitope.
ADA49636		XX Unidentified.
ADA49636		XX US200211127-A1.
ADA49636		XX PD 29-AUG-2002.
ADA49636		XX PF 27-JUN-2001; 2001US-00894018.
ADA49636		XX PR 28-DBC-1999; 99US-017330P.
ADA49636		XX PR 28-DBC-2000; 2000NG-US035568.
ADA49636		XX PR 16-APR-2001; 2001US-0284221P.
ADA49636		XX PA (SETTE/) SETTE A.
ADA49636		PA (CHES/ ) CHESNUT R.
ADA49636		PA (LIV/ ) LIVINGSTON B D.
ADA49636		PA (BAKE/ ) BAKER D M.
ADA49636		PA (NEW/ ) NEWMAN M J.

**IPS** Example 2: Col 42: 57pp; English.

**XX** The Present invention relates to peptides which induce human HER-2/neu proto-oncogene (HER-2) peptide reactive cytotoxic T-lymphocytes (CTL). The peptides are referred to as CTL-stimulating peptides. The peptides are useful for stimulating cytotoxic T-lymphocytes and generating immune responses against epitopes of proto-oncogenes. The peptides are particularly useful for treating or diagnosing various proliferative disorders (e.g. breast or ovarian cancers), or for producing anti-cancer vaccines. The Peptides may also be used as standards in the identification of small molecular-weight polypeptides, for the calibration and standardisation of chromatographic columns used in the separation of low-molecular-weight polypeptides, or as protein concentration standards in reactions. ABO07273-ABO07301 represent the CTL-stimulating Peptides of the invention.

Sequence 9 AA:	
Query	Score 41; DB 7; Length 9; Pred. No. 2e+06; Indels 0; Gaps 0;
Db	Query Match 100.0%; Score 41; Best Local Similarity 100.0%; Pred. No. 2e+06; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
	1 RLLQGETELV 9                 1 RLLQGETELV 9

RESULT 1.3	
ABW00310	ABW00310 standard; peptide; 9 AA.
ID	ABW00310
XX	ABW00310;
XX	15-JAN-2004 (first entry)
XX	HBR-2 HLA-A2 anchor peptide, HER-2:689-697.
XX	Tumour-associated antigen; proliferative disorder; cancer; vaccine; gene therapy: cytosolic; HER-2

AA Unidentified.  
DS  
KX US2003027766-A1.  
PN  
PP

PD 06-FEB-2003.  
XX 31-OCT-2001; 2001US-00001546.  
PF XX 14-MAR-1995;  
ER 95US-00403459.

(TEXA ) UNIV TEXAS SYSTEM.

WPI; 2003-765297/72.

The present invention relates to a new tumour-associated antigen (HER-1/2/neu peptide) that binds human leukocyte antigen and stimulates cytotoxic T-lymphocytes. The invention is useful for stimulating T-lymphocytes and generating immune responses against epitopes of proto-oncogenes. These are used for diagnosing and treating proliferative disorders such as cancer and for producing potential anti-cancer vaccines. The invention is claimed 4; Page 23; 59pp; English.

Query Match	100.0%	Score 41;	DB 7;	Length 9;	
Best Local Similarity	100.0%	Pred. No. 2e+05;			
Matches 9;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
1 RLLQEQELV 9					
1 RLLQEQELV 9					
RESULT 14					
DE97385	ADE97585 standard; peptide: 9 AA.				
ADE97585;					
12-FEB-2004 (first entry)					
Immunogenic HLA-A2.1 binding peptide #67.					
cytotoxic; anti-inflammatory; hepatotropic; virucide; anti-HIV; nephrotropic; neuroprotective; antiarthritic; antirheumatic; immunosuppressive; dermatological; muscular; nephrotropic; thymomimetic; haemostatic; antithyroid; antianoxic; anabolic; hypertensive; immunogenic peptide composition; immune response; prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma; cervical carcinoma; lymphoma; cytomegalovirus; CMV; condyloma acuminatum; autoimmune associated disorder; multiple sclerosis; rheumatoid arthritis; Sjogren syndrome; scleroderma; polymyositis; dermatomyositis; systemic lupus erythematosus; juvenile rheumatoid arthritis; ankylosing spondylitis; myasthenia gravis; MG; bullous pemphigoid; pemphigus; glomerulonephritis; Goodpasture's syndrome; autoimmune haemolytic anaemia; Hashimoto's disease; pernicious anaemia; idiopathic thrombocytopenic purpura; Grave's disease; Addison's disease; human leukocyte antigen A2.1; HLA A2.1; immunogenic HLA-A2.1 binding peptide.					
Synthetic.					
US2003185822-A1.					
02-OCT-2003.					
03-APR-2002; 2002US-00116557.					
05-MAR-1993; 93US-00027146.					
04-JUN-1993; 93US-000173205.					
29-NOV-1993; 93US-00119184.					
02-DEC-1994; 94US-00349177.					
(GREY H M. (SETTE A. (SIDNEY J.					
Grey HM, Sette A, Sidney J;					
WPI; 2004-041186/04.					
Immunogenic peptide composition for preventing, treating or diagnosing pathological states, e.g. prostate cancer, hepatitis B and C, Acquired Immunodeficiency Syndrome, and renal carcinoma, includes conserved residues at specified positions.					
Example 11; Page 23; 380pp; English.					
The invention describes an immunogenic peptide composition comprising 9 residues including a first conserved residue at a second position from N- terminus, and a second conserved residue at C-terminal position. The inventive peptide composition is used to elicit an immune response against a desired antigen for preventing, treating or diagnosing pathological states, e.g. prostate cancer, hepatitis B, hepatitis C, AIDS, renal carcinoma, lymphoma, cytomegalovirus (CMV), and condyloma acuminatum. It is also used to treat autoimmune					

CC associated disorders, e.g. multiple sclerosis, rheumatoid arthritis,  
 CC Sjogren syndrome, scleroderma, juvenile rheumatoid arthritis, systemic  
 CC lupus erythematosus; ankylosing spondylitis, myasthenia gravis, bullous pemphigoid, pemphigus,  
 CC glomerulonephritis, Goodpasture's syndrome, autoimmune hemolytic anemia,  
 CC Hashimoto's disease, pernicious anaemia, idiopathic thrombocytopenic  
 CC purpura, Grave's disease, and Addison's disease. The invention defines  
 CC positions within a motif enabling the selection of the peptides, which  
 CC will bind efficiently to human leukocyte antigen (HLA) A2.1. This is the  
 CC amino acid sequence of an immunogenic HLA-A2.1 binding peptide.  
 XX

SQ Sequence 9 AA;

Query Match 100.0%; Score 41; DB 8; Length 9;  
 Best Local Similarity 9; Matches 100.0%; Pred. No. 2e+06;  
 Matches 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLLQETELV 9  
 Db 1 RLLQETELV 9

RESULT 15

ADC89645

ID ADC89645 standard; peptide; 9 AA.

XX

AC ADG89645;

XX

DT 11-MAR-2004 (first entry)

XX

DB Class I HLA-restricted widely expressed antigen #10.

XX

KW metastatic cancer cell differentiation; mutated fibronectin;

XX

KW metastatic cancer; Class I HLA-restricted; widely antigen.

XX

OS Unidentified.

XX

PN WO2003100027-A2.

XX

PD 04-DEC-2003.

XX

PF 28-MAY-2003; 2003WHO-US016736.

XX

PR 28-MAY-2002; 2002US-0383530P.

XX

PA (BAYU ) BAYLOR COLLEGE MEDICINE.

XX

PI Wang R;

XX

DR 2004-035134/03.

XX

PR Identifying a cell that differentiates into a metastatic cancer cell,  
 PR useful for preventing metastatic cancer, comprises identifying a mutated  
 PR fibronectin in the cell.

XX

PS Disclosure; SEQ ID NO 88; 137pp; English.

XX

CC The invention comprises a method for identifying a cell that will  
 CC differentiate into a metastatic cancer cell, the method involves  
 CC identifying a mutated fibronectin in the cell. The method of the  
 CC invention is useful for preventing metastatic cancer. The present amino  
 CC acid sequence represents a Class I HLA-restricted widely expressed  
 CC antigen.

XX

SQ Sequence 9 AA;

Query Match 100.0%; Score 41; DB 8; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2e-06;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLLQETELV 9

Db 1 RLLQETELV 9

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: March 1, 2006, 02:48:52 ; Search time 39 Seconds  
(without alignment)  
22.204 Million cell updates/sec

Title: US-09-583-200F-22  
Perfect score: 41  
Sequence: 1 RLLQETELV 9  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters:

283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_00:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	41	100.0	1254	2	I48161	p-185 precursor -
2	41	100.0	1255	1	A24571	protein-tyrosine k
3	41	100.0	1260	1	TVRTNU	protein-tyrosine k
4	35	85.4	540	1	TVFVB	protein-tyrosine k
5	35	85.4	540	2	B44776	protein-tyrosine k
6	35	85.4	544	2	S35745	protein-tyrosine k
7	35	85.4	545	2	S00127	kinase-related tra
8	35	85.4	565	2	T46251	hypothetical prote
9	35	85.4	604	1	TVYDHH	protein-tyrosine k
10	35	85.4	698	1	TVFWLW	protein-tyrosine k
11	35	85.4	955	2	T33040	hypothetical prote
12	35	85.4	1210	1	GQHUR	epidermal growth f
13	35	85.4	1210	2	A53183	epidermal growth f
14	35	85.4	1223	1	TVCHLV	epidermal growth f
15	33	80.5	46	2	I52716	gene neu protein
16	32	78.0	416	2	B69599	- competence-damage
17	32	78.0	434	2	C71418	cytochrome P450 -
18	32	78.0	477	2	F85169	cytochrome P450 li
19	32	78.0	498	2	F84667	probable cytochrom
20	32	78.0	509	2	C85169	cytochrome P450 li
21	32	78.0	514	2	B84667	probable cytochrom
22	32	78.0	515	2	H71417	cytochrome P450 -
23	32	78.0	519	2	A96542	probable cytochrom
24	32	78.0	527	1	A71418	cytochrome P450 d1
25	32	78.0	678	2	A54514	glutamic acid-rich
26	32	78.0	738	2	A48246	ethylene-response
27	32	78.0	738	2	T01897	ethylene-response
28	32	78.0	740	2	T51619	probable ethylene
29	32	78.0	741	2	T16992	ethylene receptor

#### RESULT 1

I48161

p-185 precursor - golden hamster

C:Species: *Mesocricetus auratus* (golden hamster)  
C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 05-Oct-2004  
C:Accession: I48161

R:Nakamura, T.; Ushijima, T.; Ishizaka, Y.; Nagao, M.; Arai, M.; Yamazaki, Y.; Ishikawa, Gene 140, 251-255, 1994

A;Title: Cloning and activation of the Syrian hamster neu proto-oncogene.  
A;Reference number: I48161; PMID:94193007; PMID:7308275

A;Accession: I48161

A;Status: Preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-1254 <RES>

A;Cross-references: UNIPROT:Q60553; UNIPARC:UPI000012A111; GB:D16295; PIDN:

C:Genetics:

A;Gene: neu  
C:Superfamily: Tyrosine-protein kinase, EGF receptor type; protein kinase homology

C:Keywords: ATP  
C:Domain: protein kinase ATP-binding motif

F;718-983/Domain: protein kinase ATP-binding motif  
F;726-734/Domain: protein kinase ATP-binding motif

Query Match 100.0%; Score 41; DB 2; Length 1254;  
Best Local Similarity 100.0%; Pred. No. 2,6;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLQETELV 9  
Db 689 RLQETELV 697

#### RESULT 2

A24571

protein-tyrosine kinase (EC 2.7.1.112) erbB2 precursor - human

N;Alternate names: c-erb-B-2 protein precursor; kinase-related transforming protein erb C;Species: *Homo sapiens* (man)

C;Accession: A24571; I25491; A44188; B44188; I57622  
R;Yamamoto, T.; Ikawa, S.; Akiyama, T.; Semba, K.; Nomura, N.; Miyajima, N.; Saito, T.; Nature 319, 230-234, 1986

A;Title: Similarity of protein encoded by the human c-erb-B-2 gene to epidermal growth f A;Reference number: A24571; PMID:86118663; PMID:3003577

A;Molecule type: mRNA

A;Residues: 1-1255 <YAM>

A;Cross-references: UNIPROT:PO4626; UNIPARC:UPI000003F55F; GB:X03363; PIDN:G31197; PMID:94193009; I57622  
R;Semba, K.; Kamata, N.; Toyoshima, K.; Yamamoto, T.

Proc. Natl. Acad. Sci. U.S.A. 82, 6497-6501, 1985

A;Title: A v-erbB-related protooncogene, c-erbB-2, is distinct from the c-erbB-1/epiderm A;Reference number: A25491; PMID:86016729; PMID:2395957

A;Accession: A23491

A;Molecule type: DNA

#### ALIGNMENTS

A; Residues: 737-1031 <SEM>  
A; Cross-references: UNIPARC:UPI000016A8A7; GB: M11767; PIDN: AAA35808.1; PID: R; CCoussens, L.; Yang-Feng, T.L.; Liao, Y.C.; Chen, B.; Gray, A.; McGrath, J.; Seeburg, F  
Science 230, 1132-1139, 1985  
A; Title: Tyrosine kinase receptor with extensive homology to EGF receptor shares chromosome 11.  
A; Reference number: A44188; MUID: 86670181; PMID: 299974  
A; Accession: A44188  
A; Molecule type: DNA  
A; Cross-references: UNIPARC:UPI000016AA26; GB: M12036; PIDN: AAA35978.1; PID: R; CCoussens, L.; Yang-Feng, T.L.; Liao, Y.C.; Chen, B.; Gray, A.; McGrath, J.; Seeburg, F  
Science 230, 1132-1139, 1985  
A; Title: Tyrosine kinase receptor with extensive homology to EGF receptor shares chromosome 11.  
A; Reference number: A44188; MUID: 86670181; PMID: 299974  
A; Accession: A44188  
A; Molecule type: mRNA  
A; Residues: 1-517; 'RAUL', 522,'S', 524-654,'V', 656-1169, 'A', 1171-1555 <COU2>  
A; Cross-references: UNIPARC:UPI00001725C7; GB: M11730; PID: 9183986  
R; King, C.R.; Kraus, M.H.; Aaronson, S.A.  
A; Title: Amplification of a novel v-erbB-related gene in a human mammary carcinoma.  
A; Reference number: 159509; MUID: 8572597; PMID: 2992089  
A; Accession: I159509  
A; Status: translated from GB/EMBL/DBJ  
A; Molecule type: DNA  
A; Residues: 832-909 <REX>  
A; Cross-references: UNIPARC:UPI0000070A3F; GB: L29395; PIDN: g459807; PIDN: AAA35809.1; PID: R; Tal, M.; King, C.R.; Kraus, M.H.; Ullrich, A.; Schlessinger, J.; Givoli, D.  
Mol. Cell. Biol. 7, 2597-2601, 1987  
A; Title: Human HER2 (neu) promoter: evidence for multiple mechanisms for transcriptional control  
A; Reference number: 157622; MUID: 87286898; PMID: 3039351  
A; Accession: I157622  
A; Status: translated from GB/EMBL/DBJ  
A; Molecule type: DNA  
A; Residues: 1-191 <RL>  
A; Cross-references: UNIPARC:UPI000000427; GB: M16792; PIDN: AA58637.1; PID: C; Comment: Amplification and overexpression of this erbB-related gene occurs in about 30% of breast carcinomas  
A; Gene: GDB:ERBB2; NGU; NEU; HER-2  
A; Map Position: 17q21.1-17q21.1  
A; Introns: 25/1; 75/3; 147/1; 883/3  
A; Note: the list of introns is incomplete  
C; Function:  
C; Superfamily: Tyrosine-protein kinase, EGF receptor type; protein kinase homology domain  
C; Keywords: ATP; autophosphorylation; duplication; glycoprotein; phosphoprotein; phosphate residue  
F: 1-21/Domain: signal sequence #status predicted <SIG>  
F: 22-1255/Product: protein-tyrosine kinase erbB2 #status predicted <MAT>  
F: 22-1255/Domain: extracellular #status predicted <EXT>  
F: 70-304/Domain: EGF receptor extracellular domain repeat <EE1>  
F: 395-605/Domain: EGF receptor extracellular domain repeat <EE2>  
F: 676-1255/Domain: transmembrane #status predicted <TMM>  
F: 718-983/Domain: intracellular #status predicted <INT>  
F: 718-983/Domain: protein kinase homology <KIN>  
F: 68-124/187/Region: protein kinase ATP-binding motif  
F: 26-134/Region: protein kinase ATP-binding motif  
F: 686/Binding site: phosphate (Thr) (covalent) (by protein kinase) #status predicted  
F: 753/Active site: Lys #status predicted  
A; Residues: 100.0%; Pred. No. 2.6%; Mismatches 0; Indels 0; Gaps 0;  
A; Cross-references: UNIPROT:P11273; UNIPARC:UPI000017100D; GB: M13179; PMID: 9209679  
A; Note: the authors translated the codon AAG for residue 157 as Gly, ATG for residue 25.  
C; Genetics:  
A; Gene: erbB  
C; Superfamily: Tyrosine-protein kinase, EGF receptor type; protein kinase homology domain  
A; Residues: 1-540  
A; Cross-references: UNIPROT:P11273; UNIPARC:UPI000017100D; GB: M13179; PMID: 9209679  
A; Note: the authors translated the codon AAG for residue 157 as Gly, ATG for residue 25.  
C; Function:  
Query Match Score 41; DB 1; Length 1255;  
Best Local Similarity 100.0%; Pred. No. 2.6%; Mismatches 0; Indels 0; Gaps 0;  
Db 699 RLLQETELV 697  
Query Match Score 35; DB 1; Length 540;  
Best Local Similarity 88.9%; Pred. No. 20%; Mismatches 0; Indels 0; Gaps 0;  
Db 101 RLLQETELV 109

RESULT 3

TVTRNU  
protein-tyrosine kinase (EC 2.7.1.112) neu precursor - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 31-Dec-1988 #Sequence\_revision 31-Dec-1988 #text\_change 05-Oct-2004

**RESULT 5**  
 B44776 Protein-tyrosine kinase (EC 2.7.1.112) erbB - avian erythroblastosis virus (strain E54)  
 C.Species: avian erythroblastosis virus  
 C.Date: 28-Apr-1993 #sequence\_revision 28-Apr-1993 #text\_change 31-Dec-2004  
 R.Bruskin, A.; Jackson, J.; Bishop, J.M.; McCarley, D.J.; Schatzzman, R.C.  
 A.Title: Six amino acids from the retroviral gene gag greatly enhance the transforming protein  
 A.Reference number: A44776; MUID:90206603; PMID:1963616  
 A.Accession: B44776  
 A.Status: preliminary  
 A.Molecule type: mRNA  
 A.Residues: 1-540 <BR/>>  
 A.Cross-references: UNIPROT:Q85468; UNIPROT:Q64895; UNIPARC:UPI000017561D; GB:XS5221  
 C.Genetics:  
 A.Gene: erbB  
 C.Superfamily: protein kinase homology  
 C.Keywords: ATP; phosphotransferase; tyrosine-specific protein kinase  
 F:130-395/Domain: protein kinase ATP-binding motif  
 P:138-146/Region: protein kinase ATP-binding motif  
 Query Match 85.4%; Score 35; DB 2; Length 540;  
 Best Local Similarity 88.9%; Pred. No. 20;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 1 RLIQETEV 9  
 Db 101 RLIQERELV 109

**RESULT 6**  
 S55745 Protein-tyrosine kinase (EC 2.7.1.112) erbB - avian erythroblastosis virus  
 C.Species: avian erythroblastosis virus  
 C.Date: 03-Mar-1994 #sequence\_revision 26-May-1995 #text\_change 31-Dec-2004  
 C.Accession: S35745  
 R.Vennstrom, B.  
 Submitted to the EMBL Data Library, March 1993  
 A.Reference number: S35743  
 A.Accession: S35745  
 A.Molecule type: DNA  
 A.Residues: 1-544 <VEN>  
 A.Cross-references: UNIPROT:Q85468; UNIPROT:Q64895; UNIPARC:UPI000017561F; EMBL:X12707  
 C.Genetics:  
 A.Gene: erbB  
 C.Superfamily: protein kinase homology  
 C.Keywords: ATP; oncogene; phosphotransferase; transforming protein; tyrosine-specific  
 F:135-400/Domain: protein kinase homology <KIN>  
 F:143-151/Region: protein kinase ATP-binding motif  
 F:170/Active site: Lys #status predicted  
 Query Match 85.4%; Score 35; DB 2; Length 544;  
 Best Local Similarity 88.9%; Pred. No. 20;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

**RESULT 7**  
 S00727 kinase-related transforming protein (erbB) (EC 2.7.1.-) - avian erythroblastosis virus  
 C.Species: avian erythroblastosis virus  
 C.Date: 01-Dec-1989 #sequence\_revision 01-Dec-1989 #text\_change 31-Dec-2004  
 C.Accession: S00727  
 R.Scottling, P.; Vennstrom, B.; Jansen, M.; Graf, T.; Beug, H.; Hayman, M.J.  
 Oncogene Res. 1, 265-278, 1987  
 A.Reference number: S00727; MUID:88217326; PMID:2891102  
 A.Accession: S00727

**RESULT 5**  
 B44776 Protein-tyrosine kinase (EC 2.7.1.112) erbB - avian erythroblastosis virus (strain E54)  
 C.Species: avian erythroblastosis virus  
 C.Date: 28-Apr-1993 #sequence\_revision 28-Apr-1993 #text\_change 31-Dec-2004  
 R.Bruskin, A.; Jackson, J.; Bishop, J.M.; McCarley, D.J.; Schatzzman, R.C.  
 A.Title: Six amino acids from the retroviral gene gag greatly enhance the transforming protein  
 A.Reference number: A44776; MUID:90206603; PMID:1963616  
 A.Accession: B44776  
 A.Status: preliminary  
 A.Molecule type: mRNA  
 A.Residues: 1-540 <BR/>>  
 A.Cross-references: UNIPROT:Q85468; UNIPROT:Q64895; UNIPARC:UPI000017561B; EMBL:X06943  
 C.Genetics:  
 A.Gene: erbB  
 C.Superfamily: protein kinase homology  
 C.Keywords: ATP; phosphotransferase  
 P:135-400/Domain: protein kinase homology <KIN>  
 F:143-151/Region: protein kinase ATP-binding motif  
 Query Match 85.4%; Score 35; DB 2; Length 545;  
 Best Local Similarity 88.9%; Pred. No. 20;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 1 RLIQETEV 9  
 Db 106 RLIQERELV 114

**RESULT 8**  
 T46251 hypothetical protein DKF2p761C241.1 - human  
 C.Species: Homo sapiens (man)  
 C.Date: 04-Feb-2000 #sequence\_revision 04-Feb-2000 #text\_change 03-Jul-2004  
 C.Accession: T46251  
 R.Ottewaelder, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.  
 submitted to the Protein Sequence Database, January 2000  
 A.Reference number: 223031  
 A.Accession: T46251  
 A.Status: preliminary  
 A.Molecule type: mRNA  
 A.Residues: 1-565 <AAA>  
 A.Cross-references: UNIPROT:Q9HBM0; UNIPARC:UPI000002B6B9; EMBL:AL137497  
 A.Experiment source: adult amygdala; clone DKF2p761C241  
 C.Genetics:  
 A.Note: DKF2p761C241.1

**RESULT 9**  
 TVYUH protein-tyrosine kinase (EC 2.7.1.112) erbB - avian erythroblastosis virus (strain H)  
 C.Species: avian erythroblastosis virus  
 C.Date: 18-Apr-1984 #sequence\_revision 18-Apr-1984 #text\_change 05-Oct-2004  
 C.Accession: A00644; A38022  
 R.Yamamoto, T.; Nishida, T.; Miyajima, N.; Kawai, S.; Ooi, T.; Toyoshima, K.  
 Cell 35, 71-78, 1983  
 A.Title: The erbB gene of avian erythroblastosis virus is a member of the src gene family  
 A.Reference number: A00644; MUID:84026539; PMID:6313229  
 A.Molecule type: DNA  
 A.Residues: 1-564 <YAM>  
 A.Cross-references: UNIPROT:P00535; UNIPARC:UPI000002BA64; GB:K01216; NID:g209676; PIDN  
 R.Debuire, B.; Henry, C.; Benissa, M.; Biserte, G.; Claverie, J.M.; Saule, S.; Martin,  
 Science 224, 1456-1459, 1984  
 A.Title: Sequencing the erbB gene of avian erythroblastosis virus reveals a new type of  
 A.Reference number: A38022; MUID:84223957; PMID:6328658  
 A.Accession: A38022  
 A.Molecule type: DNA  
 A.Residues: 1-28 <W> 30-139, 'F', 141-145, 'V', 147-152 <DEB>  
 A.Cross-references: UNIPARC:UPI00001725C9; GB:K02006  
 C.Genetics:  
 A.Gene: erbB  
 C.Superfamily: Tyrosine-protein kinase, EGF receptor type; protein kinase homology  
 C.Keywords: ATP; oncogene; phosphotransferase; transforming protein; tyrosine-specific  
 F:130-395/Domain: protein kinase homology <KIN>

P;I:138-146/Region: protein kinase ATP-binding motif F;165/Active site: Lys #status predicted	Query Match	85.4%; Score 35; DB 1; Length 604; Best Local Similarity 88.9%; Pred. No. 22; Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	Qy 1 RLLQETELV 9 Db 101 RLLQBERELV 109	RESULT 10 TVFVLV protein-tyrosine kinase (EC 2.7.1.112) erbB - avian leukosis virus N; Contains: amino end of gag protein; env protein fragment; protein-tyrosine kinase C; Species: avian leukosis virus, ALV C; Accession: B00643; A00643 C; Product: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 05-Oct-2004 R; Niland, T.W.; Maroney, P.A.; Goodwin, R.G.; Rottman, F.M.; Crittenden, L.B.; Raines, M.; Haley, J.; Whittle, N.; Bennett, P.; Kinchington, D.; Ulrich, A.; Waterfield, M. A; Title: c-erbB activation in ALV-induced erythroblastosis: novel RNA processing and protein protein residues: 1-698 <NTL> A; Reference number: A00643; MUID:85228222; PMID:2968784 A; Molecule type: mRNA A; Accession: B00643 A; Comment: This protein is synthesized as a gag-env-erbB protein. C; Genetics: A; Gene: gag env-erbB C; Superfamily: Tyrosine-protein kinase, EGFR receptor type; protein kinase homology C; Keywords: ATP; oncogene; phosphotransferase; transforming protein; tyrosine-specific F P; 1-6/Product: gag protein (fragment) #status predicted <GAG> P; 7-59/Product: env protein (fragment) #status predicted <ENV> P; 194-459/Domain: protein-tyrosine kinase erbB #status predicted <ERB> P; 202-210/Region: protein kinase homology <KIN> P; 229/Active site: Lys #status predicted	Qy 1 RLLQETELV 9 Db 765 RLLQETELV 773	RESULT 12 GORUB epidermal growth factor receptor precursor - human N; Contains: protein-tyrosine kinase (EC 2.7.1.112) erbB C; Species: Homo sapiens (man) C; Accession: A00641; A25772; S30024; A38672; A00642; A43515; A23052; A05281; A60143; A37149; P.H. Nature 309, 418-425, 1984 A; Title: Human epidermal growth factor receptor cDNA sequence and aberrant expression of A; Reference number: A00641; MUID:84219729; PMID:6228312 A; Accession: A00641 A; Molecule type: mRNA A; Residues: 1-1210 <HL> A; Cross-references: UNIPROT:P00533; UNIPARC:UPI0000050F30; EMBL:X00588; PIDN:931113; PIDN:628312 A; Note: the authors translated the AAG for residue 540 as Asn R; Ishii, S.; Xu, Y.; Stratton, R.H.; Roe, B.A.; Merlino, G.T.; Pastan, I. Proc. Natl. Acad. Sci. U.S.A. 82, 4920-4924, 1985 A; Title: Characterization and sequence of the promoter region of the human epidermal growth factor receptor A; Reference number: A25772; MUID:2931899 A; Accession: A25772 A; Status: translation not shown A; Molecule type: DNA A; Residues: 1-29 <ISH> A; Cross-references: UNIPARC:UPI000016A882; GB:AAA52370-1; PIDN:9181981; PIDN:AAA52370-1; PIDN:9181981 R; Haley, J.; Whittle, N.; Bennett, P.; Kinchington, D.; Ulrich, A.; Waterfield, M. Oncogene Res. 1, 375-396, 1987 A; Title: The human RGF receptor gene: structure of the 110 kb locus and identification of A; Reference number: S30024; MUID:88217339; PMID:3329716 A; Accession: S30024 A; Molecule type: DNA A; Residues: 1-29 <HA2> A; Cross-references: UNIPARC:UPI000016A882; EMBL:X06370; PIDN:931118; PIDN:CAA29668-1; PIDN:9106777; PMID:1988448 A; Title: Contribution of new transcription and premature transcript terminal A; Reference number: A38672; MUID:91106777; PMID:1988448 A; Accession: A38672 A; Molecule type: DNA A; Residues: 1-29 <HAL> A; Cross-references: UNIPARC:UPI000016A882; GB:M38435; PIDN:AAA6171-1; PIDN:AAA6171-1 A; Experimental source: carcinoma cell line A31-7 R; Xu, Y.; Ishii, S.; Clark, A.J.L.; Sullivan, M.; Wilson, R.K.; Ma, D.P.; Roe, B.A.; Meier, R.; Lin, C.R.; Chen, W.S.; Krueger, W.; Stolarsky, L.S.; Weber, W.; Evans, R.M.; Verma, I. Science 224, 843-848, 1984 A; Title: Human epidermal growth factor receptor cDNA is homologous to a variety of RNAs A; Reference number: A00642; MUID:84245835; PMID:6330563 A; Accession: A00642 A; Molecule type: mRNA A; Residues: 'RCMWRRA', 150-187, 'KSVIQAV', 195, 'M', 197, 'A', 199-222, 'S', 224-304, 'RA', 307-322 A; Cross-references: UNIPARC:UPI00001725BD A; Experimental source: A431 human carcinoma cells, which have large numbers of EGFR receptors R; Lin, C.R.; Chen, W.S.; Krueger, W.; Stolarsky, L.S.; Weber, W.; Evans, R.M.; Verma, I. Biochem. Biophys. Res. Commun. 124, 125-132, 1984 A; Title: Expression cloning of human EGFR receptor complementary DNA: gene amplification A; Reference number: A43615; MUID:84196372; PMID:6326261 A; Accession: A43615 A; Molecule type: mRNA A; Residues: 713-964 <LIN> A; Cross-references: UNIPARC:UPI00001725BE A; Experimental source: epidermoid carcinoma cell line A431 R; Simmen, F.A.; Gope, M.L.; Schulz, T.Z.; Wright, D.A.; Carpenter, G.; O'Malley, B.W. Biochem. Biophys. Res. Commun. 124, 125-132, 1984 A; Reference number: A23062; MUID:85046483; PMID:6093780 A; Molecule type: mRNA A; Residues: 371-537 <TSP> A; Cross-references: UNIPARC:UPI0000080C1F A; Accession: T33040 A; Map position: X A; Status: preliminary A; Molecule type: DNA A; Residues: 1-955 <BN> A; Cross-references: UNIPROT:O45195; UNIPARC:UPI0000080C1F; EMBL:AF047662; PIDN: AAC04439. A; Experimental source: strain Bristol N2; clone T22B2 C; Genetics: A; Gene: CESP; T22B2.1 A; Map position: X A; Introns: 90/3; 172/3; 266/3; 670/2; 699/2; 727/2 Best Local Similarity 66.7%; Pred. No. 371; Mismatches 0; Indels 0; Gaps 0;
RESULT 11 T33040 R; Bentley, D. C; Accession: T33040 A; Description: The sequence of <i>C. elegans</i> cosmid T22B2. A; Status: submitted to the EMBL Data Library, February 1998 A; Reference number: 221267 A; Accession: T33040 A; Status: preliminary A; Molecule type: DNA A; Residues: 1-955 <BN> A; Cross-references: UNIPROT:O45195; UNIPARC:UPI0000080C1F; EMBL:AF047662; PIDN: AAC04439. A; Experimental source: strain Bristol N2; clone T22B2 C; Genetics: A; Gene: CESP; T22B2.1 A; Map position: X A; Introns: 90/3; 172/3; 266/3; 670/2; 699/2; 727/2 Best Local Similarity 66.7%; Pred. No. 371; Mismatches 0; Indels 0; Gaps 0;	Qy 1 RLLQETELV 9 Db 165 RLLQERELY 173	RESULT 11 T33040 R; Bentley, D. C; Accession: T33040 A; Description: The sequence of <i>C. elegans</i> cosmid T22B2. A; Status: submitted to the EMBL Data Library, February 1998 A; Reference number: 221267 A; Accession: T33040 A; Status: preliminary A; Molecule type: DNA A; Residues: 1-955 <BN> A; Cross-references: UNIPROT:O45195; UNIPARC:UPI0000080C1F; EMBL:AF047662; PIDN: AAC04439. A; Experimental source: strain Bristol N2; clone T22B2 C; Genetics: A; Gene: CESP; T22B2.1 A; Map position: X A; Introns: 90/3; 172/3; 266/3; 670/2; 699/2; 727/2 Best Local Similarity 66.7%; Pred. No. 371; Mismatches 0; Indels 0; Gaps 0;				

A;Residues: 1028-1210 <SIM>  
A;Cross-references: UNIPARC:UPI00001725BF  
R;Weber, W.; Gill, G.N.; Spiess, J.  
Science 224, 294-297, 1984  
A;Reference number: A05281; PMID:6324343  
A;Accession: A05281  
A;Molecule type: protein  
A;Cross-references: UNIPARC:UPI00001725C1  
R;Russell, S.; Lukas, T.J.; Cohen, S.; Staros, J.V.  
J. Biol. Chem. 260, 5205-5208, 1985  
A;Title: Identification of residues in the nucleotide binding site of the epidermal growth factor receptor from a point mutation. A Reference number: A60143; MUID:85182650; PMID:2985580  
A;Molecule type: protein  
A;Residues: 740-744, 'X', '746-747' <RUS>  
A;Cross-references: UNIPARC:UPI00001725C2  
R;Mroczkowski, B.; Moag, G.; Cohen, S.  
Nature 309, 270-273, 1984  
A;Title: ARP-stimulated interaction between epidermal growth factor receptor and supercoiled DNA: annotation, receptor activity  
A;Note: the EGF receptor (and other tyrosine kinases) can nick double-stranded DNA  
R;Chen, W.S.; Lazar, C.S.; Lund, K.A.; Welsh, J.B.; Chang, C.P.; Walton, G.M.; Der, C.J.  
Cell 59, 33-43, 1989  
A;Title: Functional independence of the epidermal growth factor receptor from a domain involved in internalization signal  
A;Reference number: A33331; MUID:90003233; PMID:2790960  
A;Comment: Binding of EGF to the receptor leads to internalization of the EGF-receptor  
C;Genetics:  
A;Gene: GDB:EGFR  
A;Cross-references: GDB:120610; OMIM:131550  
A;Map position: 7p12.3-7p12.1  
C;Keywords: Tyrosine-protein kinase, EGF receptor type; protein kinase homology  
C;Superfamily: Tyrosine-protein kinase, EGF receptor type; protein kinase homology  
C;Keywords: ATP; autophosphorylation; duplication; glycoprotein; phosphoprotein; phosphorylation  
P:1-24/Domain: signal sequence #status predicted <SIG>  
P:25-645/Domain: extracellular #status predicted <EXT>  
P:75-300/Domain: extracellular domain repeat <EB1>  
P:390-600/Domain: EGF receptor extracellular domain repeat <EB2>  
P:646-668/Domain: transmembrane #status predicted <TMM>  
P:669-1210/Domain: intracellular #status predicted <INT>  
P:710-975/Domain: protein kinase homology <KIN>  
P:999-1046/Region: coiled-coil mediated internalization signal  
P:128-175, 352, 413, 444, 528, 603/Binding site: carbohydrate (Asn) (covalent) #status predicted <CARB>  
P:745/Active site: Lys #status experimental  
Query Match Score 85.4%; Score 35; DB 1; Length 1210;  
Best Local Similarity 88.9%; Pred. No. 48;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 RLIQETELV 9  
Db 681 RLIQERELV 689

RESULT 13  
A53183 epidermal growth factor receptor precursor - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 05-Oct-2004  
R;Luetke, N.C.; Phillips, H.K.; Qiu, T.H.; Copeland, N.G.; Earp, H.S.; Jenkins, N.A.;  
Genes Dev. 8, 399-413, 1994  
A;Title: The mouse waved-2 phenotype results from a point mutation in the EGF receptor  
A;Reference number: A33183; MUID:94170986; PMID:8125255  
A;Accession: A53183  
A;Molecule type: mRNA  
A;Residues: 1-1210 <LINE>  
A;Cross-references: UNIPROT:Q01279; UNIPARC:UPI0000175614; GB:U03425  
R;Avivi, A.; Lax, I.; Ullrich, A.; Schlessinger, J.; Givol, D.; Morse, B.

Oncogene 6, 673-676, 1991  
A;Title: Comparison of EGF receptor sequences as a guide to study the ligand binding site  
A;Reference number: A43818; MUID:9132866; PMID:2030916  
A;Accession: A43818  
A;Molecule type: mRNA  
A;Residues: 1-714 <AVI>  
A;Cross-references: UNIPARC:UPI0000175615; GB:X59698  
R;Eisinger, D.P.; Serrero, G.  
Submitted to the BMBL Data Library, June 1992  
A;Accession: S24942  
A;Molecule type: mRNA  
A;Residues: 969-971, 'K', '973-1115, 'D' <EIS>  
A;Cross-references: UNIPARC:UPI0000175616; EMBL:Z12608  
R;Heisermann, G.J.; Gill, G.N.  
J. Biol. Chem. 263, 13152-13158, 1988  
A;Title: Epidermal growth factor receptor threonine and serine residues phosphorylated in mouse  
A;Reference number: A28941; PMID:88330814;  
A;Accession: A28941  
A;Molecule type: protein  
A;Residues: 689-694, 'X', '696-704, 'L', '706-707, '989-992, 'XX', '995-996, 'X', '998-1000, '1002-1009  
A;Cross-references: UNIPARC:UPI0000175617; UNIPARC:UPI0000175618; UNIPARC:UPI0000175619  
R;Hibbs, M.L.; Dunn, A.R.; Alexander, W.S.  
submitted to the BMBL Data Library, April 1994  
A;Description: The complete cDNA sequence of the Mouse Epidermal Growth Factor Receptor  
A;Reference number: S45325  
A;Accession: S45325  
A;Status: Preliminary  
A;Molecule type: DNA  
A;Residues: 1-97, 'K', '973-1210 <VER>  
A;Cross-references: UNIPARC:UPI00002182B; EMBL:X78987; PIDN:CA455587.1; P  
R;Corria, B.C.; Das, S.K.; Andrews, G.K.; Dey, S.K.  
Proc. Natl. Acad. Sci. U.S.A. 90, 55-59, 1993  
A;Title: Expression of the epidermal growth factor receptor gene is regulated in mouse  
A;Reference number: I49643; MUID:93126380; PMID:7678348  
A;Accession: I49643  
A;Status: transcribed from GB/EMBL/DDJB  
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A;Cross-references: UNIPARC:UPI000016CD26; GB:L06864; PIDN:gi13001; PIDN:gi13001; PID  
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A;Gene: EGFR  
C;Superfamily: Tyrosine-protein kinase, EGF receptor type; protein kinase homology  
C;Keywords: ATP; growth factor receptor; kinase-related transforming protein; phosphoprotein  
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F:712-977/Domain: protein kinase homology <KIN>  
F:720-728/Region: protein kinase ATP-binding motif  
F:680-695/Binding site: phosphate (Thr) (covalent) #status experimental  
F:697,1070,1071/Binding site: phosphate (Ser) (covalent) #status experimental  
F:993/Binding site: (or 103 or 1032) phosphate (Ser) (covalent) #status experimental  
F:11197/Binding site: phosphate (Tyr) (covalent) #status experimental  
Query Match Score 88.4%; Pred. No. 48;  
Best Local Similarity 88.9%; Pred. No. 48;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULTS 14  
TVCHLV  
epidermal growth factor receptor precursor - chicken  
C;Species: Gallus gallus (chicken)  
C;Accession: A27720; A00633  
C;Date: 28-Feb-1986 #sequence\_revision 05-May-1995 #text\_change 05-Oct-2004  
R;Ax, I.; Johnson, A.; Howk, R.; Sap, J.; Bellot, F.; Winkler, M.; Ullrich, A.; Venet, N.;  
Mol. Cell. Biol. 8, 1970-1978, 1988  
A;Title: Chicken epidermal growth factor (EGF) receptor: cDNA cloning, expression in mo

A;Reference number: A27720; MUID:88261272; PMID:3260329  
A;Accession: A27720  
A;Molecule type: mRNA  
A;Residues: 1-1223 <LAX>  
A;Cross-references: UNIPARC:P00534; UNIPARC:UPI00001725C3; GB:M20386  
R;Nilsen, T.W.; Maroney, P.A.; Goodwin, R.G.; Rottman, F.M.; Crittenden, L.B.; Raines, M  
Cell 41, 719-726, 1985  
A;Title: c-erbB activation in ALV-induced erythroblastosis: novel RNA processing and pro  
A;Reference number: A00643; MUID:85223222; PMID:298784  
A;Accession: A00643  
A;Molecule type: mRNA  
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A;Cross-references: UNIPARC:UPI00001725C4; GB:M10066  
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A;Gene: erbB  
C;Superfamily: Tyrosine-protein kinase, EGFR receptor type; protein kinase homology  
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specific protein kinase  
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P;31-1223/Product: epidermal growth factor receptor #status predicted <EGF>  
P;81-307/Domain: extracellular #status predicted <ECI>  
P;397-610/Domain: EGFR receptor extracellular domain repeat <EE1>  
P;655-677/Domain: transmembrane #status predicted <TM>  
P;678-1223/Domain: intracellular #status predicted <INT>  
P;719-984/Domain: protein kinase homology <KIN>  
P;727-735/Region: protein kinase ATP-binding motif  
P;136,205,360,370,422,575,580,615,635/Binding site: carbohydrate (Thr) (covalent) #  
P;192,650/Binding site: carbohydrate (Ser) (covalent) #status predicted  
P;687/Banding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted  
P;754/Active site: Lys #status predicted  
P;1100,1183,1208/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #stat  
Query Match 85.4%; Score 35; DB 1; Length 1223;  
Best Local Similarity 88.9%; Pred. No. 48;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 RLLQETELV 9  
Db 690 RLLQERELV 698

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RESULT 15  
I52716  
Gene neu protein - hamster (fragment)  
C;Species: Cricetinae gen. sp. (hamster)  
C;Date: 12-Aug-1996 #sequence\_revision 12-Aug-1996 #text\_change 05-Oct-2004  
C;Accession: I52716  
R;Nakamura, T.; Ishijima, T.; Ishizaka, Y.; Nagao, M.; Nemoto, T.; Hara, M.; Ishikawa, T  
Cancer Res. 54, 976-980, 1994  
A;Title: neu proto-oncogene mutation is specific for the neurofibromas in a N-nitroso-N-  
A;Reference number: I52716; MUID:94147418; PMID:7906199  
A;Status: Preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
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Best Local Similarity 100.0%; Pred. No. 3.6;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RLLQETE 7  
Db 40 RLLQTE 46

GenCore version 5.1.7  
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## OM protein - protein search, using sw model

Run on: March 1, 2006, 02:46:52 ; Search time 227 Seconds  
 (without alignments)  
 27.972 Million cell updates/sec

Title: US-09-583-200F-22  
 Perfect score: 41  
 Sequence: 1 RLLQETELV 9

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 70528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_5.80.\*  
 1: uniprot\_sprot:  
 2: uniprot\_trembl:  
 \* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	41	100.0	36	2	Q9NP09_HUMAN	Q9NP09 homo sapien
2	41	100.0	304	2	Q68KJ7_FELICA	Q68KJ7 felis silv
3	41	100.0	435	2	Q62M04_HUMAN	Q62M04 homo sapien
4	41	100.0	881	2	Q8C0B7_MOUSE	Q8C0B7 mmu muscu
5	41	100.0	1254	1	ERBB2_TESAN	Q65M53 mesocricetu
6	41	100.0	1255	1	ERBB2_HUMAN	P04626 homo sapien
7	41	100.0	1257	1	ERBB2_RAT	P06494 rattus norv
8	41	100.0	1259	1	ERBB2_CANFA	Q18735 canis famil
9	41	100.0	1259	2	Q8K3F9_RAT	Q8A3F9 rattus norv
10	41	100.0	1305	2	O6ZP00_MOUSE	O6ZP00 mus musculu
11	35	85.4	202	2	O6CP04_CANFA	Q5dt04 canis famil
12	35	85.4	276	2	Q8BYB4_MOUSE	Q8Byb4 mus musculu
13	35	85.4	540	1	ERBB_AVIRE	P11273 avian erych
14	35	85.4	545	1	O85468_MOUSE	Q85468 avian erych
15	35	85.4	567	2	Q86714_AVVER	Q86714 avian rou-
16	35	85.4	604	1	ERBB_AVIRE	P00534 avian erych
17	35	85.4	634	1	ERBB_ALV	P00534 avian leuko
18	35	85.4	639	2	Q8BBT2_MOUSE	Q8By12 mus musculu
19	35	85.4	703	1	EGFR_CHICK	P13387 gallus gall
20	35	85.4	729	2	Q86712_AVVER	Q86712 avian rou-
21	35	85.4	731	2	Q6P1Q3_HUMAN	Q6P1Q3 homo sapien
22	35	85.4	731	2	Q5RF17_PONPY	O8rf17 pongo pygma
23	35	85.4	774	2	Q6PCG6_XENLA	Q5pcg6 xenopus lae
24	35	85.4	779	1	VEZA_HUMAN	Q9bam0 homo sapien
25	35	85.4	780	2	Q8BZB5_MOUSE	Q8Bzbs5 mus musculu
26	35	85.4	782	2	Q5X152_RAT	Q5ti52 rattus norv
27	35	85.4	955	2	O45195_CAEEL	Q45195 caenorhabdi
28	35	85.4	962	2	O64895_ERETR	Q64895 avian erych
29	35	85.4	1081	2	O59P18_HUMAN	Q59P18 homo sapien
30	35	85.4	1091	2	Q5O4U8_HUMAN	Q5O4U8 homo sapien
31	35	85.4	1094	2	Q4RWY4_TETNG	Q4rwY4 tetracodon n

## RESULT 1

Q9NP09\_HUMAN PRELIMINARY;  
 ID Q9NP09; AC Q9NP09; DT 01-OCT-2000 (TREMBLrel. 15, Created); DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update); DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update); DB ERBB2 (Fragment); GN Name=ERBB2;

OS Homo sapiens (Human); OC Bokaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; OC Homo; OC NCBI\_TaxID=9606;

RN [1]; RP NUCLEOTIDE SEQUENCE; RC TISSUE-Placenta;

RX MEDLINE=94169396; PubMed=7907235; DR Briscoe W.T., Ray D.B., Airhart J.L., Ratliff A.L., Shockley B.A., Whetell L., Schaefer F.V., Williams R.M.; FT NON-TER DR M86910; AAF30295.1; -; Genomic\_DNA; RT "A new high frequency polymorphism in the HER-2/neu oncogene in normal tissue and breast tumors."; RL Breast Cancer Res. Treat. 28:45-49 (1993).

FT NON-TER DR M86910; AAF30295.1; -; Genomic\_DNA; SQ SEQUENCE 36 AA; 36 AA; 4204 MW; 230DA20B669867DS CRC64;

Query Match Score 10.0%; Best Local Similarity 10.0%; Matches 9; Conservative 0; Gaps 0; Indels 0;

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Query Match Score 41; DB 2; Length 36; Best Local Similarity 10.0%; Pred. No. 0.4; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DR M86910; AAF30295.1; -; Genomic\_DNA; FT NON-TER DR M86910; AAF30295.1; -; Genomic\_DNA; SQ SEQUENCE 36 AA; 36 AA; 4204 MW; 230DA20B669867DS CRC64;

RA	Biolatti B., Di Renzo M.F.; "Spontaneous Feline Carcinoma Is a Model of HER2 Overexpressing Poor Prognosis Human Breast Cancer.", <i>Cancer Res.</i> 65: 907-912 (2005).	DR InterPro; IPR002290; Ser_thr_pkinase.
RT	"Spontaneous Feline Carcinoma Is a Model of HER2 Overexpressing Poor Prognosis Human Breast Cancer.", <i>Cancer Res.</i> 65: 907-912 (2005).	DR InterPro; IPR002290; Ser_thr_pkinase.
RL	EMBL: A1685128; AAU01910.1; - ; Genomic_DNA.	DR PRINTS; PRO0353; 4FB4SRDXIN.
DR	SMBR; Q6BKJ7; 57-304.	DR ProdDom; PD000001; Prot_kinase; 1.
DR	GO; GO:0005524; F:ATP binding; IEA.	DR SMART; SM00261; FU; 2.
DR	GO; GO:0004674; F:protein-threonine kinase activity; IEA.	DR SMART; SM00219; STTKC; 1.
DR	GO; GO:0004733; F:protein-Tyrosine kinase activity; IEA.	DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR	GO; GO:0016740; F:Transferase activity; IEA.	DR PROSITE; PSS0011; PROTEIN_KINASE_DOM; 1.
DR	GO; GO:0006468; P:protein amino acid phosphorylation; IEA.	DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR	InterPro; IPR000719; Prot_kinase.	KW Kinase; Receptor; Tyrosine-Protein kinase.
DR	InterPro; IPR002290; Ser_thr_pkinase.	SQ SEQUENCE 435 AA; 47891 MW; 1FA846710D31311A CRC64;
DR	InterPro; IPR002245; Tyr_pkinase.	Query Match 100.0%; Score 41; DB 2; Length 435;
DR	INTERPRO; PR0008266; Tyr_pkinase_AS.	Best Local Similarity 10.0%; Pred. No. 5.7;
DR	PRODOM; PD000001; Prot_kinase; 1.	Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DR	SMART; SM00220; S_TTKC; 1.	
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.	
DR	PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.	
DR	PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.	
DR	ATP binding; Kinase; Nucleotide-binding; Transferase.	
FT	NON_TER 1 304	RESULT 4 Q8GC07_MOUSE ID Q8GC07_MOUSE_PRELIMINARY; PRT; 881 AA.
FT	SEQUENCE 304 AA; 33934 MW; 47C0290F4BC020ED CRC64;	AC Q8GC07; 23 , Created)
DR	Query Match 100.0%; Score 41; DB 2; Length 304;	DT 01-MAR-2003 (TREMBLrel. 23 , Last annotation update)
DR	Best Local Similarity 100.0%; Pred. No. 3.9;	DT 01-MAR-2004 (TREMBLrel. 26 , Last annotation update)
DR	Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	DE Mus_musculus 13 days embryo male testis cDNA, RIKEN full-length enriched library, clone:603044908 Product: v-erb-b2 erythroblastic DE leukemia viral oncogene homolog 2, neuro/glioblastoma derived oncogene DS homolog (avian), full insert sequence. (Fragment).
DR	Qy 1 RLLQETELV 9	OS Mus_musculus (Mouse).
Db	42 RLLQETELV 50	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; OC Mammalia; Eutheria; Euarchontoglires; Gires; Rodentia; Sciurognathi; OC Muridae; Murinae; Mus.
GN	Name=Erbb2;	OX NCBI_TaxID=10909;
GN	Mus_musculus (Mouse).	RN [1]
NCBI_TAXID		RN NUCLEOTIDE_SEQUENCE.
NCBI_TAXID		RC STRAIN=C57BL/6J; TISSUE=Testis;
NCBI_TAXID		RC MEDLINE=21085660; PubMedID=11217051; DOI=10.1038/35055500;
NCBI_TAXID		RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
NCBI_TAXID		RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
NCBI_TAXID		RA Aizawa K., Izawa M., Nishi K., Kyosawa H., Kondo S., Yamanaoka I.,
NCBI_TAXID		RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
NCBI_TAXID		RA Kadota K., Matsuda M.A., Ashburner M., Batalov S., Casavant T.,
NCBI_TAXID		RA Fleischmann W., Gaasterland T., Gibbs C., King B., Kochiwa H.,
NCBI_TAXID		RA Kuehl P., Lewis S., Matsuo Y., Nikaldo I., Pesole G., Quackenbush J.,
NCBI_TAXID		RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner U., Washio T.,
NCBI_TAXID		RA Sakai K., Okido T., Furuno M., Aono H., Barsh G.,
NCBI_TAXID		RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
NCBI_TAXID		RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
NCBI_TAXID		RA Gustincich S., Hill D., Holmann M., Kamiya M., Lee N.H.,
NCBI_TAXID		RA Lyons P., Marchionni L., Mashima J., Mazzarelli P., Mombaerts P.,
NCBI_TAXID		RA Nordone P., Ring B., Rodriguez J., Sakamoto N.,
NCBI_TAXID		RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibusawa Y., Storch K.-P.,
NCBI_TAXID		RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
NCBI_TAXID		RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Hayashizaki Y.;
NCBI_TAXID		RT "Functional annotation of a full-length mouse cDNA collection."
NCBI_TAXID		RN Nature 409: 685-690 (2001).
NCBI_TAXID		RP NUCLEOTIDE_SEQUENCE.

RC	STRAIN=C57BL/6J; TISSUE=Testis;	SQ	SEQUENCE	881 AA;	97501 MW;	5D5042BE9F8F0836 CRC64;
RA	the RIKEN Genome Exploration Research Group Phase I & II Team;					
RA	"Analysis of the mouse transcriptome based on functional annotation of					
RT	67,770 full-length cDNAs."					
RL	Nature 420:563-573 (2002).					
[4]						
RN	NUCLEOTIDE SEQUENCE.					
RC	STRAIN=C57BL/6J; TISSUE=Testis;					
RX	Medline:1049374; Pubmed:11041539; DOI:10.1101/gr.145100;					
RA	Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,					
RA	Konno H., Okazaki Y., Muranatsu M., Hayashizaki Y.,					
RT	"Normalization and subtraction of cap-trapper-selected cDNAs to					
RT	prepare full-length cDNA libraries for rapid discovery of new genes."					
RL	Genome Res. 10:1617-1630 (2000).					
RN	[5]					
RP	NUCLEOTIDE SEQUENCE.					
RC	STRAIN=C57BL/6J; TISSUE=Testis;					
RX	Medline:10530913; Pubmed:11076861; DOI:10.1101/gr.152600;					
RA	Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,					
RA	Konno H., Akiyama J., Nishi K., Kitsumai T., Tashiro H., Itoh M.,					
RA	Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,					
RA	Fujikawa S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,					
RA	Yoneda Y., Ishikawa T., Ozawa K., Taraka T., Matsubara S., Kawai J.,					
RA	Okazaki Y., Muranatsu M., Inoue Y., Kira A., Hayashizaki Y.,					
RT	"RIKEN integrated sequence analysis (RISA) system-384-format					
RT	sequencing pipeline with 384 multicapillary sequencer."					
RL	Genome Res. 10:1757-1771 (2000).					
RN	[6]					
RC	NUCLEOTIDE SEQUENCE.					
RC	STRAIN=C57BL/6J; TISSUE=Testis;					
RA	Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,					
RA	Fukuda S., Furuno M., Hanazono K., Hiraoka T., Hirozane T.,					
RA	Hayashida K., Hattatsu M., Hiramoto K., Hiraoka T., Hori F., Imotsu K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,					
RA	Katoh H., Kawai J., Kojima H., Kondo S., Konno H., Kouda M., Koya S.,					
RA	Kurihara C., Matsumura T., Miyazaki A., Murata M., Nakamura M.,					
RA	Nishi K., Nomura K., Numazaki R., Ohno M., Onsato N., Okazaki Y.,					
RA	Saitoh H., Sakai C., Sakai K., Sasaki N., Sano H., Sasaki D., Shibata K., Shiragawa A., Shizaki T., Sogabe Y., Tagami M.,					
RA	Togawa A., Takahashi P., Takaku-Akaiwa S., Takeda Y., Tanaka T.,					
RA	Submitted (JUL-2001) to the EMBL/GenBank/DBJ/GenBank databases.					
DR	EMBL; AK031342; BAC2742.1; -; mRNA.					
DR	HSRP; P06494; INRY.					
DR	Ensembl; ENSEMBL; OBC007; 1-255.					
DR	MGI; MGI:95410; Erbb2.					
DR	GO; GO:0001624; Caprical plasma membrane; IDA.					
DR	GO; GO:0005137; C:cytoplasm; IDA.					
DR	GO; GO:0005515; F:protein binding; IDI.					
DR	GO; GO:0007507; P:heart development; IMP.					
DR	GO; GO:0042522; P:myelination; IMP.					
DR	GO; GO:007422; P:peripheral nervous system development; IMP.					
DR	InterPro; IPR000094; EGFR_L.					
DR	InterPro; IPR00612; Furin repeat.					
DR	InterPro; IPR000119; Prot kinase.					
DR	InterPro; IPR001245; Tyr_Pkinase.					
DR	InterPro; IPR00836; Tyr_Pkinase_AS.					
DR	InterPro; IPR004019; YLP motif.					
DR	Pfam; PF01030; Recep_L_domain; 1.					
DR	Pfam; PF02757; YLP; 2.					
DR	PRINTS; PR00109; TYRKINASE.					
DR	P-Dom; PD000001; Prot_kinase; 1.					
DR	SMART; SM00261; FU; 2.					
DR	SMART; SM00219; TyrKCI; 1.					
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.					
DR	PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.					
DR	ATP-binding_Kinase; PROTEIN_KINASE_TYR; 1.					
KW	Tyrosine-protein kinase.					
FT	NON_TER					

RESULT 5  
 ERBB2 MESAU  
 ID ERBB2 MESAU  
 AC Q60553;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DE Receptor tyrosine-protein kinase erbB-2 precursor (EC 2.7.1.112)  
 DS (p185erbB2) (C-erbB-2) (NEU proto-oncogene).  
 GN Name=ERBB2; Synonyms=NEU;  
 OS Mesocricetus auratus (Golden hamster).  
 OC Metacarca; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muricoidea; Criceridae; Cricetinae; Mesocricetus.  
 [1]  
 NCBI\_TaxID=1036; RN  
 RC TISSUE=Nerve;  
 RX MEDLINE=94193007; PubMed=7908275; DOI=10.1016/0378-1119(94)9053-3;  
 RA Nakamura T., Ushijima T., Ishizaka Y., Nagao M., Arai M., Yamazaki Y.,  
 RA Ishikawa T.;  
 RT "Cloning and activation of the Syrian hamster neu proto-oncogene."  
 RL Gene 140:251-255(1994).  
 CC -I- FUNCTION: Essential component of a neuregulin-receptor complex,  
 although neuregulins do not interact with it alone. GP30 is a  
 potential ligand for this receptor. Not activated by EGF, TGF-  
 alpha and amphiregulin (By similarity).  
 CC -I- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein  
 tyrosine phosphate.  
 CC -I- SUBUNIT: Heterodimer with each of the other ERBB receptors  
 (Potential). Part of a complex with EGFR and either PIK3CA or  
 PIK3CB. Interacts with PRKCBP and PLXNB1. May interact with  
 PIK3CB when phosphorylated on Tyr-1196 (By similarity).  
 CC -I- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -I- PTM: Ligand-binding increases phosphorylation on tyrosine  
 residues.  
 CC -I- SIMILARITY: Belongs to the Tyr protein kinase family. EGF receptor  
 subfamily.

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 use as long as its content is in no way modified and this statement is not  
 removed.

CC EMBL; D16235; BAA03801.1; -; mRNA.  
 DR PIR; I48161; I48161.  
 DR HSSP; P06494; 1NBY.  
 DR SMR; Q60553; 23-629.  
 DR InterPro; IPR000494; EGFR\_L.  
 DR InterPro; IPR006211; Furin-like.  
 DR InterPro; IPR006212; Furin repeat.  
 DR PIR; IPR00719; Prot\_Kinase.  
 DR InterPro; IPR001245; Tyr\_Pkinase.  
 DR InterPro; IPR008266; Tyr\_Pkinase\_AS.  
 DR InterPro; IPR004019; YLP motif.  
 DR Pfam; PF00757; Furin\_Like\_1.  
 DR Pfam; PF01030; Recep\_L\_domain.  
 DR Pfam; PF02757; YLP; 2.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR SMART; SM00261; FU; 2.  
 DR SMART; SM00219; TyrKCI; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR ATP-binding\_Kinase; PROTEIN\_KINASE\_TYR; 1.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR ProdDom; PD000001; Prot\_kinase; 1.  
 DR SMART; SM00261; FU; 1.

DR	SMART; SM00219; TYRK; 1.	GN	Name=ERBB2; Synonyms=HER2, NEU, NGL;
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.	OS	Homo sapiens (Human)
DR	PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
DR	PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.	OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
KW	Nucleotide-binding; Disease mutation; Glycoprotein; Kinase; Multigene family;	OC	Homo.
KW	Nucleotide-binding; Phosphorylation; Proto-oncogene; Receptor; Signal;	OC	NCBP1_TaxID=9606;
KW	Transferase; Transmembrane; Tyrosine-protein kinase.	OX	RN
FT	SIGNAL 1 21	[1]	NUCLEOTIDE SEQUENCE.
FT	CHAIN 22 1254	RP	NUCLEOTIDE SEQUENCE. PubMed=1003577;
FT	TOPO DOM 22 652	RX	Medline=86118663; PubMed=2999974;
FT	TRANSMEM 653 675	RA	Yamamoto T., Ikawa S., Akiyama T., Semba K., Nomura N., Miyajima N., Saito T., Toyoshima K.;
FT	TOPO DOM 676 1254	RA	Seuberg P.H., Liebermann T.A., Schlessinger J., Francke U., Levinson A., Ulrich A.;
FT	DOMAIN 720 987	RT	"Similarity of protein encoded by the human c-erb-B-2 gene to epidermal growth factor receptor.";
FT	NP_BIND 726 734	RT	"Tyrosine kinase receptor with extensive homology to EGFR receptor shares chromosomal location with neu oncogene.";
FT	REGION 1195 1197	RN	[2]
FT	COMBIAIS 158 368	RP	NUCLEOTIDE SEQUENCE, AND VARIANT ALA-1170.
FT	COMBIAIS 472 644	RX	Medline=86070181; PubMed=2999974;
FT	ACT SITE 845 945	RA	Coussens L., Yang-Peng T.L., Liao Y.C., Chen E., Gray A., McGrath J., Seuberg P.H., Liebermann T.A., Schlessinger J., Francke U.,
FT	BINDING 753 753	RA	"Similarity of protein encoded by the human c-erb-B-2 gene to epidermal growth factor receptor.";
FT	MOD_RES 1139 1139	RT	"Tyrosine kinase receptor with extensive homology to EGFR receptor shares chromosomal location with neu oncogene.";
FT	MOD_RES 1196 1196	RN	[2]
FT	MOD_RES 1247 1247	RP	NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND VARIANTS CYS-452; VAL-655 AND CYS-rich.
FT	CARBOHYD 68 68	RX	Medline=86010701; PubMed=2999974;
FT	CARBOHYD 125 125	RA	Rieder M.J., Livingston R.J., Daniels M.R., Montoya M.A., Chung M.-W., Miyamoto K.B., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D., Schwickitz W.S., Sherwood J.K., Witruk L.A., Nickerson D.A.;
FT	CARBOHYD 187 187	RA	"Human HER2 (neu) promoter: evidence for multiple mechanisms for transcriptional initiation.";
FT	CARBOHYD 259 259	RT	"NIHHS-SNPs, environmental genome project, NIHHS ES15478, Department of Genome Sciences, Seattle, WA (URL: http://egg.gs.washington.edu).";
FT	CARBOHYD 530 530	RT	Submitted (DBC-2002) to the EMBL/GenBank/DBJ databases.
FT	CARBOHYD 571 571	RL	[3]
FT	CARBOHYD 629 629	RP	NUCLEOTIDE SEQUENCE OF [GENOMIC DNA].
FT	DISULFID 195 204	RX	Medline=86010701; PubMed=2999974;
FT	DISULFID 199 212	RA	Rieder M.J., Livingston R.J., Daniels M.R., Montoya M.A., Chung M.-W., Miyamoto K.B., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D., Schwickitz W.S., Sherwood J.K., Witruk L.A., Nickerson D.A.;
FT	DISULFID 236 244	RA	"Human HER2 (neu) promoter: evidence for multiple mechanisms for transcriptional initiation.";
FT	DISULFID 240 252	RT	"A v-erbB-related protooncogene, c-erbB-2, is distinct from the C-erbB-1/epidermal growth factor receptor gene and is amplified in a human salivary gland adenocarcinoma";
FT	DISULFID 255 264	RT	RT
FT	DISULFID 268 295	RT	RT
FT	DISULFID 299 311	RT	RT
FT	DISULFID 315 331	RT	RT
FT	DISULFID 334 338	RT	RT
FT	DISULFID 511 520	RT	RT
FT	DISULFID 515 528	RT	RT
FT	DISULFID 531 540	RT	RT
FT	DISULFID 544 560	RT	RT
FT	DISULFID 563 576	RT	RT
FT	DISULFID 567 584	RT	RT
FT	DISULFID 587 596	RT	RT
FT	DISULFID 600 623	RT	RT
FT	DISULFID 626 634	RT	RT
FT	DISULFID 630 642	RT	RT
FT	VARIANT 658 658	RT	RT
FT	VARIANT 659 659	RT	RT
SQ	SEQUENCE 1254 AA; 138253 MW; 974C3791C21F2BE1 CRC64;	RT	RT
Query Match	100.0%	RT	RT
Best Local Similarity	100.0%	RT	RT
Matches	9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	RT	RT
Qy	1 RLLQETELV 9	RT	RT
Db	689 RLLQETELV 697	RT	RT
RESULT 6	NUCLEOTIDE SEQUENCE OF 1081-1245, AND VARIANT ALA-1170.	RT	RT
ID ERBB2_HUMAN STANDARD; Q142556; Q6DV1; Q9UMK4;	RP	RT	RT
ID ERBB2_HUMAN STANDARD; Q142556; Q6DV1; Q9UMK4;	RP	RP	RP
AC P044256; Q142556; Q6DV1; Q9UMK4;	RP	RP	RP
DT 13-AUG-1987 (Rel. 05, Created)	RP	RP	RP
DT 13-AUG-1987 (Rel. 05, Last sequence update)	RP	RP	RP
DT 13-SEP-2005 (Rel. 48, Last annotation update)	RP	RP	RP
DE Receptor tyrosine-protein kinase erbB-2 precursor (EC 2.7.1.112)	RP	RP	RP
DE (p155erbB2) (C-erbB-2) (NEU proto-oncogene) (Tyrosine kinase-type cell surface receptor HER2) (MLN 19).	RP	RP	RP

RX	PubMed=15210733; DOI=10.1083/jcb.2003112094;	DR	PDB: 1OVC; Model: A=737-1031.
RA	Swiercz J.M., Kuner R.; Offermanns S.;	DR	PDB: 1S78; X-ray; A=B=23-646.
RT	"Plexin-B1/RhoG-mediated RhoA activation involves the receptor tyrosine kinase Erbb2.";	DR	Ensembl; ENSG0000011736; Homo sapiens.
RU	J. Cell. Biol. 165:869-880 (2004).	DR	HGNC: HGNC-3430; ERBB2.
RW	[110]	DR	MIM: 164870;
RP	X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 654-662 IN COMPLEX WITH HLA AND BETA-2 MICROGLOBULIN; PubMed=10593938; DOI=10.1074/jbc.274.51.36422;	DR	GO: 00016021; C:integral to membrane; NAS.
RM	MEDLINE=20052861; PubMed=10593938;	DR	GO: 0005886; C:plasma membrane; Factor receptor activity; NAS.
RA	Kuhns J.J., Batalia M.A., Yan S., Collins E.J.; RT	DR	GO: 0005006; F:epidermal growth factor receptor binding; TAS.
RA	"Poor binding of a HER-2/neu epitope (GP2) to HLA-A2.1 is due to a lack of interactions with the center of the peptide.";	DR	GO: 0043125; F:protein heterodimerization activity; NAS.
RT	RT	DR	GO: 0004716; F:receptor signaling protein tyrosine kinase . . . ; TAS.
RL	J. Biol. Chem. 274:36422-36427 (1999).	DR	GO: 0008283; F:cell proliferation; TAS.
RN	[111]	DR	GO: 0007507; F:heart development; TAS.
RP	X-RAY CRYSTALLOGRAPHY (2.52 ANGSTROMS) OF 23-529 IN COMPLEX WITH FAB.	DR	GO: 0030879; F: mammary gland development; TAS.
RX	MEDLINE=93497871; PubMed=12610529; DOI=10.1038/nature01392;	DR	GO: 00048015; F: phosphoinositide-mediated signaling; NAS.
RA	Cho H.-S., Mason K., Ramyar K.X., Stanley A.M., Gabelli S.B., Denney D.W. Jr., Leahy D.J.; RT	DR	GO: 0006468; F:protein amino acid phosphorylation; TAS.
RA	"Structure of the extracellular region of HER2 alone and in complex with the Herceptin Fab.";	DR	GO: 0045765; F:regulation of angiogenesis; NAS.
RT	RT	DR	GO: 0007169; F:transmembrane receptor protein tyrosine kin. . . ; NAS.
RL	Nature 421:756-760 (2003).	DR	InterPro: IPR000494; EGFR_L.
RN	[112]	DR	InterPro: IPR006211; Furin-like.
RP	VARIANTS VAL-654 AND VAL-655.	DR	InterPro: IPR006212; Furin repeat.
RX	MEDLINE=93194196; PubMed=895488;	DR	InterPro: IPR000719; Prot_Kinase.
RA	Ehsani A., Low J., Wallace R.B., Wu A.M.; RT	DR	InterPro: IPR001245; Tyr_DKinase.
RA	"Characterization of a new allele of the human ERBB2 gene by allele-specific competition hybridization.";	DR	InterPro: IPR008266; Tyr_pkInase_AS.
RP	Genomics 15:426-429 (1993).	DR	InterPro: IPR0004019; YLP motif.
CC	-I- FUNCTION: Essential component of a neuregulin-receptor complex, although neuregulins do not interact with it alone. GP30 is a potential ligand for this receptor. Not activated by EGFR, TGF- $\alpha$ , alba and ambiregulin.	DR	PFam; PF00757; Furin-like; 1.
CC	-I- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein tyrosine Phosphate.	DR	PFam; PF01030; Recpt_L_domain; 2.
CC	-I- SUBUNIT: Heterodimer with each of the other ERBB receptors (Potential). Interacts with PRKCBAP (By similarity). Binds PLXNB1.	DR	PRINTS; PRO0109; TYRKINASE.
CC	Part of a complex with EGFR and either PIK3C2A or PIK3C2B. May interact with PIK3C2B when phosphorylated at Tyr-1196.	DR	PRODom; PD000001; Prot_kinase; 1.
CC	-I- SUBCELLULAR LOCATION: Type I membrane protein.	DR	SMART; SM00261; FU; 3.
CC	-I- PTM: Ligand-binding increases phosphorylation on tyrosine residues (By similarity).	DR	SMART; SM00219; Tyrcc; 1.
CC	-I- POLYMORPHISM: There are fours alleles due to the variations in positions 654 and 655. Allele B1 (Ile-654/Ile-655) has a frequency of 0.78; allele B2 (Ile-654/Val-655) has a frequency of 0.206; allele B3 (Val-654/Val-655) has a frequency of 0.012.	DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
CC	-I- SIMILARITY: Belongs to the Tyr protein kinase family. EGF receptor subfamily.	DR	PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
CC	CC	DR	PROSITE; PS00109; PROTEIN_KINASE_TTR; 1.
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.	DR	KW Nucleotide-binding; Glycoprotein_Kinase; Multigene Family; Nucleotide-binding; Phosphorylation; Polymorphism; Receptor; Signal; Transferase; Transmembrane; Tyrosine-protein kinase.
CC	CC	FT SIGNAL	FT SIGNAL
CC	CC	FT CHAIN	FT CHAIN
CC	CC	FT TOPO_DOM	FT TOPO_DOM
CC	CC	FT TRANSMEM	FT TRANSMEM
CC	CC	FT DOMAIN	FT DOMAIN
CC	CC	FT DOMAIN	FT DOMAIN
CC	CC	FT NP_BIND	FT NP_BIND
CC	CC	1 21	1 21
CC	CC	22	22
CC	CC	652	652
CC	CC	653	675
CC	CC	676	1255
CC	CC	720	987
CC	CC	726	734
CC	CC	ATP (By similarity).	ATP (By similarity).
CC	CC	Query Match Score 41; DB 1; Length 1255;	Query Match Score 41; DB 1; Length 1255;
CC	CC	Best Local Similarity 100.0%; Pred. No. 18;	Best Local Similarity 100.0%; Pred. No. 18;
CC	CC	Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC	CC	Qy 1 RLLQETELV 9	Qy 1 RLLQETELV 9
CC	CC	Db 689 RLLQETELV 697	Db 689 RLLQETELV 697
<b>RESULT 7</b>			
ERBB2	ERBB2 RAT	ID P06497; Q6P732; STANDARD; PRT; 1257 AA.	
ERBB2	ERBB2 RAT	AC P06497; Q6P732; STANDARD; PRT; 1257 AA.	
ERBB2	ERBB2 RAT	DT 01-JAN-1998 (Rel. 06, Created)	
ERBB2	ERBB2 RAT	DT 15-DEC-1998 (Rel. 37, Last sequence update)	
ERBB2	ERBB2 RAT	DT 13-SEP-2005 (Rel. 48, Last annotation update)	
ERBB2	ERBB2 RAT	DE Receptor_tyrosine-protein_kinase_ERBB_2 precursor (EC 2.7.1.112)	
ERBB2	ERBB2 RAT	DE (p185erbB2) (C-erbB2) (NEU proto-oncogene)	
ERBB2	ERBB2 RAT	DE Receptor-related protein.	
ERBB2	ERBB2 RAT	DE Name=erbB2; Synonyms=Neu;	
ERBB2	ERBB2 RAT	GN Rat	
ERBB2	ERBB2 RAT	OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;	
ERBB2	ERBB2 RAT	OC Muroidea; Euarchontoglires; Gires; Rodentia; Sciurognathi;	
ERBB2	ERBB2 RAT	OC Muridae; Muridae; Murinae; Rattus.	
ERBB2	ERBB2 RAT	OC NCB_I_TaxID=10116;	
ERBB2	ERBB2 RAT	RN [1]	

RP	NUCLEOTIDE SEQUENCE.	DR	InterPro; IPR001245; Tyr_Dkinase.
RC	TISSUE=Prostate;	DR	InterPro; IPR003266; Tyr_Dkinase_AS.
RC	MEDLINE=86118662; PubMed=3945311;	DR	InterPro; IPR004019; YLP_Motif.
RA	Bargmann C.I., Hung M.-C., Weinberg R.A.;"	DR	Fram; PF00157; Furin-like; 1.
RA	"The neu oncogene encodes an epidermal growth factor receptor-related	DR	PROSITE; PS00105; Recep_L_domain; 2.
[3]	protein.";	DR	PFam; PF02757; YLP; 2.
RT	protein".;	DR	PRINTS; PRO0109; TYRKINASE.
RL	Nature 319:226-230(1986).	DR	ProdDom; PD000001; Prot_kinase; 1.
RN	[2]	DR	SMART; SM00261; FU; 4.
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE mRNA].	DR	SMART; SM00219; TyrKc; 1.
RC	TISSUE=Prostate;	DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
RG	NIH - Mammalian Gene Collection (MGC) Project;	DR	PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
RL	Submitted (NOV-2003) to the EMBL/Genbank/DBJ databases.	DR	PROSITE; PS00108; PROTEIN_KINASE_TIR; 1.
RN	[3]	KW	3D-structure; ATP-binding; Disease mutation; Glycoprotein; Kinase.
RP	NUCLEOTIDE SEQUENCE OF 634-699.	KW	Multigenic family; Nucleotide-binding; Phosphorylation; Proto-oncogene.
BX	MEDLINE=92035293; PubMed=1662063;	KW	Receptor; Signal; Transferase; Transmembrane; Tyrosine-protein kinase erbB-2.
RA	Masui T., Maun A.M., Macatoo T.L., Garland B.M., Okamura T.,	FT	Receptor_tyrosine-protein_kinase_erbB-2.
RA	Smith R.A., Cohen S.M.;	FT	Signal; 1
RT	"Direct DNA sequencing of the rat neu oncogene transmembrane domain	FT	TOPODOM
RT	reveals no mutation in urinary bladder carcinomas induced by N-butyryl	FT	TOPODOM
RT	thiazoylformamide or N-methyl-N-nitrosourea.",	FT	TOPODOM
RT	N-[4-(5-nitro-2-furyl)-2-	FT	TOPODOM
RT	thiazoyl]formamide or N-methyl-N-nitrosourea.,";	FT	TOPODOM
RT	carcinogenesis 12:1975-1978(1991).	FT	TOPODOM
[4]		FT	TOPODOM
RP	NUCLEOTIDE SEQUENCE OF 852-905.	FT	TOPODOM
RC	TISSUE=Sciatic nerve;	FT	TOPODOM
RX	MEDLINE=92122556; PubMed=2025425; DOI=10.1016/0896-6273(91)90167-X;	FT	TOPODOM
RA	Lai C., Lemke G.;	FT	TOPODOM
RA	"An extended family of protein-tyrosine kinase genes differentially	FT	TOPODOM
RT	expressed in the vertebrate nervous system.";	FT	TOPODOM
RT	Neuron 6:691-704(1991).	FT	TOPODOM
RN	[5]	FT	TOPODOM
RP	STRUCTURE BY NMR OF 650-668.	FT	TOPODOM
RX	MEDLINE=92155181; PubMed=1346763;	FT	TOPODOM
RA	Gullick W.J., Bottcomley A.C., Loats F.J., Doak D.G., Mulvey D.,	FT	CARBODY
RA	Ram R., Crumpton M.J., Sternberg M.J.E., Campbell I.D.;	FT	CARBODY
RT	"Three dimensional structure of the proto-oncogenic and oncogenic forms of the neu protein.";	FT	CARBODY
RT	EMBO J. 11:43-48 (1992).	FT	CARBODY
CC	-1- FUNCTION: Essential component of a neuregulin-receptor complex,	FT	CARBODY
CC	although neuregulins do not interact with it alone. GP30 is a	FT	CARBODY
CC	potential ligand for this receptor. Not activated by EGF, TGF-	FT	CARBODY
CC	alpha and amphiregulin.	FT	CARBODY
CC	-1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein	FT	CARBODY
CC	-1- SUBUNIT: Heterodimer with each of the other ERBB receptors. The	FT	CARBODY
CC	constitutively activated oncogenic variant forms a homodimer.	FT	CARBODY
CC	Interacts with PRKCBP and PRKCB. Part of a complex with EGFR and	FT	CARBODY
CC	either PIK3CA or PIK3CB. May interact with PIK3C2B when	FT	CARBODY
CC	phosphorylated on Tyr-119. (By similarity)	FT	CARBODY
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein.	FT	CARBODY
CC	-1- PMM: Ligand-binding increases phosphorylation on tyrosine residues	FT	CARBODY
CC	(By similarity).	FT	CARBODY
CC	-1- SIMILARITY: Belongs to the Tyr protein kinase family. EGF receptor	FT	CARBODY
CC	subfamily.	FT	CARBODY
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration	FT	CARBODY
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -	FT	CARBODY
CC	the European Bioinformatics Institute. There are no restrictions on its	FT	CARBODY
CC	use as long as its content is in no way modified and this statement is not	FT	CARBODY
CC	removed.	FT	CARBODY
DR	EMBL; X03362; CAA7059_1; AUT INIT; mRNA.	FT	V > E (in oncogenic NEU).
DR	PIR; A22562; TVRNU.	FT	S -> G (in Ref. 2).
DR	PDB; 1NBY; X-ray; C=23-631.	FT	LCVSS -> CGIE (in Ref. 2).
DR	Ensembl; ENSEMBL:ENSG0000006450; Rattus norvegicus.	FT	Score 41; DB 1; Length 1257;
DR	RGD; 2561; Erbb.	FT	Best Local Similarity 100.0%; Pred. No. 18;
DR	GO; GO:0045525; P: regulation of cell proliferation; TAS.	FT	Mismatches 0; Indels 0; Gaps 0;
DR	InterPro; IPR00044; EGFR_L.	Qy	1 RIUQETELV 9
DR	InterPro; IPR006211; Furin-like.	Db	691 RIUQETELV 699
DR	InterPro; IPR006212; Furin repeat.		
DR	InterPro; IPR00719; Prot_Finase.		



DR	GO:0005006; P:epidermal growth factor receptor activity; IEA.	DR	InterPro; IPR002290; Ser-thr_Pkinase.
DR	GO:0006468; P:protein amino acid phosphorylation; IEA.	DR	InterPro; IPR001245; Tyr_Pkinase.
DR	GO:0007169; P:transmembrane receptor protein tyrosine kin. . ; IEA.	DR	InterPro; IPR008266; Tyr_Pkinase_AS.
DR	InterPro; IPR002048; EF-hand.	DR	InterPro; IPR004019; YLP motif.
DR	InterPro; IPR000494; EGFR_L.	DR	Pfam; PF00757; Furin-like.
DR	InterPro; IPR06211; Furin-repeat.	DR	Pfam; PF01030; Recp_L-domain;
DR	InterPro; IPR006212; Furin-repeat.	DR	Pfam; PF02157; YLP_2.
DR	InterPro; IPR000719; Prot_Fkinase.	DR	PRINTS; PRO0109; TYRKINASE.
DR	InterPro; IPR01245; Tyr_Pkinase.	DR	ProdDom; PD000001; Prot_kinase; 1.
DR	InterPro; IPR008266; Tyr_Pkinase_AS.	DR	SMART; SM0261; FU; 4.
DR	InterPro; IPR004019; YLP motif.	DR	SMART; SM00220; S_TKc; 1.
DR	Pfam; PF00757; Furin-like; 1.	DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR	Pfam; PF01030; Recp_L-domain; 2.	DR	PROSITE; PS00101; PROTEIN_KINASE_TYR; 1.
DR	Pfam; PF02157; YLP_2.	DR	PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR	PRINTS; PRO0109; TYRKINASE.	KW	ATP-binding; Kinase; Nucleotide-Binding; Transferase.
DR	PRODom; PD000001; Prot_kinase; 1.	FT	NON_TER 1 1
DR	SMART; SM00261; FU; 4.	SQ	SEQUENCE 1305 AA; 143508 MW; A51D897408521860 CRC64;
DR	SMART; SM00219; TYRK_C; 1.	Query	1 RLLQETELV 9
DR	PROSITE; PS00018; EF HAND; UNKNOWN 1.	Match	100.0%; Score 41; DB 2; Length 1305;
DR	PROSITE; PS50011; PROTEIN_KINASE_ATP; 1.	Best Local Similarity	100.0%; Pred. No. 19;
DR	PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.	Matches	9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DR	SEQUENCE 1259 AA; 139101 MW; B724BD5CC33A8953 CRC64;	Db	739 RLLQETELV 747
Query	1 RLLQETELV 9	RESULT 11	Q6QT04 CANPA
Db	693 RLLQETELV 701	ID	Q6QT04_CANPA PRELIMINARY; PRT; 202 AA.
AC		AC	Q6QT04; AC
DR		DR	Q6QT04; DT
DR	05-JUL-2004 (TRMBLrel. 27, Created)	DT	05-JUL-2004 (TRMBLrel. 27, Created)
DR	05-JUL-2004 (TRMBLrel. 27, Last sequence update)	DT	05-JUL-2004 (TRMBLrel. 27, Last sequence update)
DR	05-JUL-2004 (TRMBLrel. 27, Last annotation update)	DT	05-JUL-2004 (TRMBLrel. 27, Last annotation update)
DR	MKIAA3023 protein (Fragment)	DE	Epidermal growth factor receptor (fragment).
GN	Name=Erbb2; Synonyms=mKIAA3023;	GN	Name=EGFR;
OS	Mus musculus (Mouse).	OS	Canis familiaris (Dog).
OC	Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Muroidea; Muridae; Murinae; Mus.	OC	Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OX		OX	Canis.
NCBI_TaxID=10090;		NCBI_TaxID=9615;	NCBI_TaxID=9615;
RN		RN	[1]_NUCLEOTIDE_SEQUENCE.
RA		RA	Dickinson, P.J.; Roberts, B.N.; Mallen-StClair J.; Leutenegger C.M., LeCouteur R.A.;
RL		RL	Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR		DR	EMBL; AY527212; AAS1799.0.1; - mRNA.
DR		DR	SMR; Q6QT04; 85-202.
DR		DR	Ensembl; ENSCAFG0000003455; Canis familiaris.
DR		DR	GO; GO-000524; F:ATP binding; IEA.
DR		DR	GO; GO-0004713; F:protein-tyrosine kinase activity; IEA.
DR		DR	GO; GO-0004872; F:receptor activity; IEA.
DR		DR	GO; GO-0006468; P:protein amino acid phosphorylation; IEA.
DR		DR	InterPro; IPR000719; Prot_kinase.
FT		FT	Non_TER 1 1
SQ		SQ	SEQUENCE 202 AA; 22140 MW; 4CBBBCD0514FF1EE CRC64;
Query	1 RLLQETELV 9	Query	1 RLLQETELV 9
Db	70 RLLQETELV 78	Match	85.4%; Score 35; DB 2; Length 202;
AC		Best Local Similarity	88.9%; Pred. No. 50;
DR		Matches	8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;



DR InterPro; IPR001245; Tyr kinase.  
 DR InterPro; IPR008266; Tyr kinase\_AS.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR ProDom; PD000001; Prot kinase; 1.  
 DR SMART; SM00219; TyrKc; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
 DR ATP-binding; Kinase; Nucleotide-Binding; Oncogene; Phosphorylation.  
 KW Transferase; Tyrosine-protein kinase.  
 DOMAIN 132 399 Protein kinase.  
 FT NP BIND 138 146 ATP (By similarity).  
 FT ACT SITE 257 257 By similarity.  
 FT BINDING 165 165 ATP (By similarity).  
 FT VARIANT 270 270 H -> D (In thermotable v-erbB).  
 SQ SEQUENCE 540 AA; 60413 MW; 5B53297AA069B65D CRC64;  
 Query Match 85.4%; Score 35; DB 1; Length 540;  
 Best Local Similarity 88.9%; Pred. No. 1.4e+02;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 1 RLLQFTELY 9  
 Db 101 RLLQFRELV 109

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RESULT 14  
 Q85468\_98BTR\_9RTR PRELIMINARY; PRT; 545 AA.  
 ID Q85468\_9RTR PRELIMINARY; PRT; 545 AA.  
 AC Q85468\_9RTR PRELIMINARY; PRT; 545 AA.  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
 DB (tb4) v-erbB gene (Fragment).  
 OS Avian erythroblastosis virus.  
 OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;  
 OC Alpharetrovirus.  
 NCBI\_TaxID=11861;  
 RN  
 RP NUCLEOTIDE SEQUENCE.  
 MEDLINE=88217326; PubMed=2897102;  
 RA Scutting P.; Venstrom B.; Janzen M.; Graf T.; Beug H.; Haymann M.J.;  
 RT "Common site of mutation in the erbB gene of avian erythroblastosis  
 virus mutants that are temperature sensitive for transformation.";  
 RL Oncogene Res. 1:265-278(1987).  
 [2]  
 RN NUCLEOTIDE SEQUENCE.  
 MEDLINE=2020603; PubMed=1969616;  
 RA Bruskin A.; Jackson J.; Bishop J.M.; McCarley D.J.; Schatzman R.C.;  
 RT "Six amino acids from the retroviral gene gag greatly enhance the  
 transforming potential of the oncogene v-erb-B";  
 RL Oncogene 5:15-24 (1990).  
 DR EMBL; X05943; CAA30024.1; -; Genomic\_DNA.  
 PIR; B44776; B44776.  
 DR PIR; S00727; S00727.  
 DR HSSP; Q8H2C9; 1M17.  
 DR SMART; SM00468; 121-444.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.  
 DR GO; GO:0016740; F:transferase activity; IEA.  
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
 DR InterPro; IPR000719; Prot kinase.  
 DR InterPro; IPR001245; Tyr\_P kinase.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR ProDom; PD000001; Prot\_kinase; 1.  
 DR SMART; SM00219; TyrKc; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
 DR ATP-binding; Kinase; Nucleotide-Binding; Oncogene; Transf erase;  
 KW Tyrosine-protein kinase.

Query Match 85.4%; Score 35; DB 2; Length 567;  
 Best Local Similarity 88.9%; Pred. No. 1.5e+02;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RLLQFTELY 9  
 Db 106 RLLQFRELV 114

Search completed: March 1, 2006, 02:50:48  
 Job time : 229 secs

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Run on:	March 1, 2006, 03:02:52 ; Search time 19 Seconds (without alignments)	Total number of hits satisfying chosen parameters: 117670	Minimum DB seq length: 0 Maximum DB seq length: 2000000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	RESULT 1 US-11-033-039-608 ; Sequence 608, Application US/11033039 ; Publication No. US20060002947A1 ; GENERAL INFORMATION: ; APPLICANT: HUMPHREYS, ROBERT ; INVENTION: LI-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES ; FILE REFERENCE: REH-2017US01 ; CURRENT APPLICATION NUMBER: US/11/033,039 ; CURRENT FILING DATE: 2005-01-11 ; PRIOR APPLICATION NUMBER: 10/245,871 ; PRIOR FILING DATE: 2002-09-17 ; PRIORITY NUMBER: 10/197,000 ; PRIORITY FILING DATE: 2002-07-17 ; PRIOR APPLICATION NUMBER: 09/396,813 ; PRIOR FILING DATE: 1999-09-14 ; NUMBER OF SEQ ID NOS: 1452 ; SOFTWARE: PatentIn version 3.3 ; SEQ ID NO 608 ; LENGTH: 9 ; TYPE: PRT ; ORGANISM: Homo sapiens US-11-033-039-608
Database :	Published Applications_AAA_New: 1: /cggn2_6/ptodata/2/pubbaa/US08 NEW PUB.pep.* 2: /cggn2_6/ptodata/2/pubbaa/US06 NEW PUB.pep.* 3: /cggn2_6/ptodata/2/pubbaa/US07 NEW PUB.pep.* 4: /cggn2_6/ptodata/2/pubbaa/PCT NEW PUB.pep.* 5: /cggn2_6/ptodata/2/pubbaa/US05 NEW PUB.pep.* 6: /cggn2_6/ptodata/2/pubbaa/US10 NEW PUB.pep.* 7: /cggn2_6/ptodata/2/pubbaa/US11 NEW PUB.pep.* 8: /cggn2_6/ptodata/2/pubbaa/US60 NEW PUB.pep.*	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.			
				SUMMARIES	
Result No.	Score	Query Match Length DB ID	Description		
1	41	100.0 9 US-11-033-039-608	Sequence 608, APP		
2	41	100.0 9 US-11-033-039-614	Sequence 614, APP		
3	41	100.0 1255 6 US-10-770-726-62	Sequence 62, Appl		
4	41	100.0 1255 7 US-11-022-562-213	Sequence 213, APP		
5	41	100.0 1255 7 US-11-113-202-10	Sequence 10, Appl		
6	41	100.0 1255 7 US-11-033-039-553	Sequence 553, APP		
7	41	100.0 1255 7 US-11-153-288-9	Sequence 9, Appl		
8	41	100.0 1255 7 US-11-202-516-4	Sequence 4, Appl		
9	41	100.0 1255 7 US-11-175-405-2	Sequence 2, Appl		
10	41	100.0 1258 7 US-11-033-039-930	Sequence 930, APP		
11	35	85.4 943 7 US-11-113-202-8	Sequence 8, Appl		
12	35	85.4 1210 7 US-11-113-202-6	Sequence 6, Appl		
13	35	85.4 1210 7 US-11-145-566-1	Sequence 1, Appl		
14	32	78.0 738 7 US-11-140-625-11	Sequence 11, Appl		
15	32	78.0 738 7 US-11-140-625-13	Sequence 13, Appl		
16	32	78.0 738 7 US-11-140-625-12	Sequence 12, Appl		
17	31	75.6 1308 6 US-10-912-971-12	Sequence 12, Appl		
18	31	75.6 1308 7 US-11-113-202-16	Sequence 16, Appl		
19	29	70.7 549 6 US-10-467-657-4612	Sequence 4612, AP		
20	29	70.7 549 6 US-10-467-657-7190	Sequence 7190, AP		
21	29	70.7 754 7 US-11-140-625-10	Sequence 10, Appl		
22	29	70.7 3674 7 US-11-000-463-454	Sequence 454, APP		
23	28	68.3 209 6 US-10-519-390-3	Sequence 3, Appl		
24	28	68.3 209 7 US-11-176-830-203	Sequence 203, APP		
25	28	68.3 209 7 US-11-176-830-401	Sequence 401, APP		

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; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396,813
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 1452
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO: 614
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-033-039-614

Query Match          100.0%;  Score 41;  DB 7;  Length 1255;
Best Local Similarity      100.0%;  Pred. No. 1;
Matches   9;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;
Qy      1 RLLQETELV 9
Db      689 RLLQETELV 697

RESULT 3
US-10-770-726-62
; Sequence 62, Application US/10770726
; Publication No. US20050266409A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; FILE REFERENCE: AM101079 (031896-01000)
; CURRENT APPLICATION NUMBER: US10/770,726
; CURRENT FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 48440
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 62
; LENGTH: 1255
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-770-726-62

Query Match          100.0%;  Score 41;  DB 7;  Length 1255;
Best Local Similarity      100.0%;  Pred. No. 1;
Matches   9;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;
Qy      1 RLLQETELV 9
Db      689 RLLQETELV 697

RESULT 4
US-11-022-562-213
; Sequence 213, Application US/11022562
; Publication No. US20050249742A1
; GENERAL INFORMATION:
; APPLICANT: Ruprecht, Ruth M.
; APPLICANT: Shisong, Jiang
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING
; TITLE OF INVENTION: A CYTOTOXIC T LYMPHOCYTE IMMUNE RESPONSE
; FILE REFERENCE: DFN-043CN
; CURRENT APPLICATION NUMBER: US11/022,562
; CURRENT FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: PCT/US03/20322
; PRIOR FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: 60/392718
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 213
; LENGTH: 1255
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-022-562-213

Query Match          100.0%;  Score 41;  DB 7;  Length 1255;
Best Local Similarity      100.0%;  Pred. No. 1;
Matches   9;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;
Qy      1 RLLQETELV 9

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RESULT 7  
 Db 689 RLLQETELV 697  
 Qy 1 RLLQETELV 9  
 Db 689 RLLQETELV 697

RESULT 9  
 US-11-155-208-9 Application US/11155288  
 ; Sequence 9, Application US/11155288  
 ; Publication No. US20060008468A1  
 ; GENERAL INFORMATION  
 ; APPLICANT: Simard, Chih-Sheng  
 ; TITLE OF INVENTION: COMBINATIONS OF TUMOR-ASSOCIATED  
 ; TITLE OF INVENTION: BEATRICE CLAUDIA  
 ; FILE REFERENCE: MANK 050A  
 ; CURRENT APPLICATION NUMBER: US/11/155,288  
 ; CURRENT FILING DATE: 2005-06-17  
 ; PRIOR APPLICATION NUMBER: 60/580,969  
 ; PRIOR FILING DATE: 2004-06-17  
 ; NUMBER OF SEQ ID NOS: 40  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO 9  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-11-155-208-9

Query Match 100.0%; Score 41; DB 7; Length 1255;  
 Best Local Similarity 100.0%; Pred. No. 1;  
 Matches 9; Conservative 0; Mismatches 0; Gaps 0;  
 Indels 0; Gaps 0;

Qy 1 RLLQETELV 9  
 Db 689 RLLQETELV 697

RESULT 8  
 US-11-202-516-4  
 ; Sequence 4, Application US/11202516  
 ; Publication No. US20060008465A1  
 ; GENERAL INFORMATION  
 ; APPLICANT: Steinaa, Lucilla  
 ; APPLICANT: Mouritzen, Soren  
 ; APPLICANT: Gautam, Anand  
 ; APPLICANT: Dalum, Iben  
 ; APPLICANT: Haaning, Jesper  
 ; APPLICANT: Leach, Dana  
 ; APPLICANT: Nielsen, Klaus  
 ; APPLICANT: Karlsson, Gunilla  
 ; APPLICANT: Rasmussen, Peter  
 ; TITLE OF INVENTION: Novel Methods for Therapeutic Vaccination  
 ; FILE REFERENCE: 4614-0107PUS2  
 ; CURRENT APPLICATION NUMBER: US/11/202,516  
 ; PRIOR APPLICATION NUMBER: US 09/606,703  
 ; PRIOR FILING DATE: 2001-04-04  
 ; PRIOR APPLICATION NUMBER: PCT/DK99/00525  
 ; PRIOR FILING DATE: 1999-10-05  
 ; PRIOR APPLICATION NUMBER: DK 1998 01261  
 ; PRIOR FILING DATE: 1998-10-05  
 ; PRIOR APPLICATION NUMBER: US 60/105,011  
 ; PRIOR FILING DATE: 1998-10-20  
 ; NUMBER OF SEQ ID NOS: 33  
 ; SOFTWARE: Patentin version 3.0  
 ; SEQ ID NO 4  
 ; LENGTH: 1255  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-11-202-516-4

Query Match 100.0%; Score 41; DB 7; Length 1255;  
 Best Local Similarity 100.0%; Pred. No. 1;  
 Matches 9; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 RLLQETELV 9  
 Db 689 RLLQETELV 697

RESULT 10  
 US-11-033-039-930  
 ; Sequence 930, Application US/11033039  
 ; Publication No. US20060002947A1  
 ; GENERAL INFORMATION  
 ; APPLICANT: HUMPHREYS, ROBERT  
 ; APPLICANT: XU, MINZHEN  
 ; TITLE OF INVENTION: LI-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES  
 ; FILE REFERENCE: REH-2017US01  
 ; CURRENT APPLICATION NUMBER: US/11/033,039  
 ; CURRENT FILING DATE: 2005-01-11  
 ; PRIOR APPLICATION NUMBER: 10/245,871  
 ; PRIOR FILING DATE: 2002-09-17  
 ; PRIOR APPLICATION NUMBER: 10/197,000  
 ; PRIOR FILING DATE: 2002-07-17  
 ; PRIOR APPLICATION NUMBER: 09/396,813  
 ; PRIOR FILING DATE: 1999-09-14  
 ; NUMBER OF SEQ ID NOS: 1452  
 ; SOFTWARE: Patentin version 3.3  
 ; SEQ ID NO 930  
 ; LENGTH: 1255  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-11-033-039-930

Query Match 100.0%; Score 41; DB 7; Length 1258;  
 Best Local Similarity 100.0%; Pred. No. 1;  
 Matches 9; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 RLLQETELV 9  
 Db 689 RLLQETELV 697

RESULT 11  
 US-11-113-202-8

Sequence 8, Application US/11113202  
; GENERAL INFORMATION: Publication No. US20050272637A1  
; APPLICANT: Clinton, Gail M.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING SIGNALING BY IGF-1  
; FILE REFERENCE: 49321-136  
; CURRENT APPLICATION NUMBER: US/11113202  
; CURRENT FILING DATE: 2005-04-22  
; PRIOR APPLICATION NUMBER: US 60/590,473  
; PRIOR FILING DATE: 2004-07-23  
; PRIOR APPLICATION NUMBER: US 60/564,893  
; PRIOR FILING DATE: 2004-04-22  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO: 8  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-113-202-8

Query Match 85.4%; Score 35; DB 7; Length 943;  
Best Local Similarity 88.9%; Pred. No. 13; Indels 1; Gaps 0;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RLLQETELV 9  
Db 414 RLLQERELV 422

RESULT 12  
US-11-113-202-6  
; Sequence 6, Application US/11113202  
; GENERAL INFORMATION: Publication No. US20050272637A1  
; APPLICANT: Clinton, Gail M.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING SIGNALING BY IGF-1  
; FILE REFERENCE: 49321-136  
; CURRENT APPLICATION NUMBER: US/11113202  
; CURRENT FILING DATE: 2005-04-22  
; PRIOR APPLICATION NUMBER: US 60/590,473  
; PRIOR FILING DATE: 2004-07-23  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO: 6  
; LENGTH: 1210  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-113-202-6

Query Match 85.4%; Score 35; DB 7; Length 1210;  
Best Local Similarity 88.9%; Pred. No. 17; Indels 1; Gaps 0;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RLLQETELV 9  
Db 681 RLLQERELV 689

RESULT 15  
US-11-140-625-13  
; Sequence 13, Application US/111140625  
; GENERAL INFORMATION: Publication No. US20060026706A1  
; APPLICANT: Van Wezel, Gilles P.  
; TITLE OF INVENTION: A method for marker-less integration of a sequence of interest  
; FILE REFERENCE: P62377SUS00  
; CURRENT APPLICATION NUMBER: US/11/140,625  
; CURRENT FILING DATE: 2005-05-27  
; PRIOR APPLICATION NUMBER: EP 020800000 9  
; PRIOR FILING DATE: 2002-11-28  
; PRIOR APPLICATION NUMBER: PCT/NL2003/000835  
; PRIOR FILING DATE: 2003-11-27  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO: 11  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: ETR1 homologue derived from Nicotiana tabacum  
US-11-140-625-11

Query Match 78.0%; Score 32; DB 7; Length 738;  
Best Local Similarity 100.0%; Pred. No. 42; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LIQETEL 8  
Db 366 LIQETEL 372

RESULT 13  
US-11-145-566-1  
; Sequence 1, Application US/11114566  
; GENERAL INFORMATION: Publication No. US20050272083A1  
; APPLICANT: SOMASEKAR SESHAGIRI  
; TITLE OF INVENTION: EGFR Mutations  
; FILE REFERENCE: 39766-0153  
; CURRENT APPLICATION NUMBER: US/11/145,566

; PRIOR FILING DATE: 2003-11-27  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO: 13  
; LENGTH: 738  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: ETR1 homologue derived from *Arabidopsis thaliana*  
US-11-140-625-13

Query Match 78.0%; Score 32; DB 7; Length 738;  
Best Local Similarity 100.0%; Pred. No. 42;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LLQTEL 8

Db 368 LLQTEL 374

Search completed: March 1, 2006, 03:05:52  
Job time : 19 secs

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Result No.	Score	Query Match	Length	DB ID	Description
1	41	100.0	9	2 US-08-812-393A-52	Sequence 52, Appl Sequence 6, Appl
2	41	100.0	9	3 US-09-354-533-6	Sequence 6, Appl
3	41	100.0	9	3 US-09-894-018-320	Sequence 52, Appl Sequence 52, Appl Sequence 26, Appl
4	41	100.0	9	3 US-09-774-681-52	Sequence 26, Appl
5	41	100.0	9	4 US-10-001-546-26	Sequence 40, Appl
6	41	100.0	9	4 US-10-080-013-40	Sequence 41, Appl
7	41	100.0	9	4 US-10-245-871-608	Sequence 608, Appl
8	41	100.0	9	4 US-10-245-871-614	Sequence 614, Appl
9	41	100.0	9	4 US-10-149-138-671	Sequence 671, Appl
10	41	100.0	9	4 US-10-149-138-676	Sequence 671, Appl
11	41	100.0	9	4 US-10-149-138-2276	Sequence 2276, Ap
12	41	100.0	9	4 US-10-149-138-4420	Sequence 4420, Ap
13	41	100.0	9	4 US-10-441-161-88	Sequence 88, Appl
14	41	100.0	9	4 US-10-253-286-608	Sequence 608, Appl
15	41	100.0	9	4 US-10-253-286-614	Sequence 614, Appl
16	41	100.0	9	4 US-10-289-566-41	Sequence 41, Appl
17	41	100.0	9	4 US-10-333-430-65	Sequence 65, Appl
18	41	100.0	9	4 US-10-641-005-6	Sequence 6, Appl
19	41	100.0	9	4 US-10-149-138-671	Sequence 671, Appl
20	41	100.0	9	4 US-10-149-138-2276	Sequence 2276, Ap
21	41	100.0	9	4 US-10-149-138-4420	Sequence 4420, Ap
22	41	100.0	9	5 US-10-474-960A-320	Sequence 320, Appl
23	41	100.0	9	5 US-10-865-113A-9	Sequence 9, Appl
24	41	100.0	9	6 US-11-120-347-6	Sequence 6, Appl
25	41	100.0	15	3 US-09-354-533-40	Sequence 40, Appl
26	41	100.0	15	3 US-10-149-138-3869	Sequence 3869, Ap
27	41	100.0	15	4 US-10-149-138-3927	Sequence 3927, Ap

Qy 1 RLLQETELV 9  
 Db 1 RLLQETELV 9

RESULT 2  
 US-09-354-533-6  
 ; Sequence 6, Application US/09354533  
 ; Publication No. US2002005561441  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cheever, Martin A.  
 ; DISCLOSURE: Mary L.  
 ; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN  
 ; FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE  
 ; HER-2/neu ONCOGENE IS ASSOCIATED

NUMBER OF SEQUENCES: 69  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Seed and Berry LLP  
 STREET: 6300 Columbia Center, 701 Fifth Avenue  
 CITY: Seattle  
 STATE: Washington  
 COUNTRY: US  
 ZIP: 98104-7092

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/354,533  
 FILING DATE: 15-Jul-1999  
 CLASSIFICATION: <Unknown>  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Sharkey, Richard G.  
 REGISTRATION NUMBER: 32,629  
 REFERENCE/DOCKET NUMBER: 920010.448C9  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (206) 622-4900  
 TELEFAX: (206) 682-6031  
 INFORMATION FOR SEQ ID NO: 6:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 9 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
 US-09-354-533-6

Query Match 100.0%; Score 41; DB 3; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLLQETELV 9  
 Db 1 RLLQETELV 9

RESULT 3  
 US-09-894-018-320  
 ; Sequence 320, Application US/09894018  
 ; Patent No. US20020119127A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: EPIMMUNE, Inc.  
 ; APPLICANT: Sette, Alessandro  
 ; APPLICANT: Chestnut, Robert  
 ; APPLICANT: Livingston, Brian  
 ; APPLICANT: Baker, Denis W  
 ; APPLICANT: Newman, Mark  
 ; APPLICANT: Brown, David  
 ; TITLE OF INVENTION: METHODS AND SYSTEM FOR OPTIMIZING  
 ; MINIGENES AND PEPTIDES THEREBY  
 ; FILE REFERENCE: 39963-20033.00  
 ; CURRENT APPLICATION NUMBER: US/09/894,018  
 ; CURRENT FILING DATE: 2001-06-27

Query Match 100.0%; Score 41; DB 3; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLLQETELV 9  
 Db 1 RLLQETELV 9

RESULT 4  
 US-09-774-681-52  
 ; Sequence 52, Application US/09774681  
 ; Publication No. US20030208780A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Sunol Molecular Corporation  
 ; APPLICANT: Sherman, Linda  
 ; APPLICANT: Lustgarten, Joseph  
 ; TITLE OF INVENTION: RECOMBINANT CONSTRUCTS ENCODING T CELL  
 ; TUMOR ANTIGENS  
 ; FILE REFERENCE: 31333-200101  
 ; CURRENT APPLICATION NUMBER: US/09/774,681  
 ; CURRENT FILING DATE: 2001-02-01  
 ; PRIOR APPLICATION NUMBER: US 08/812,393  
 ; PRIOR FILING DATE: 1997-03-15  
 ; PRIOR APPLICATION NUMBER: US 60/012,845  
 ; PRIOR FILING DATE: 1998-03-05  
 ; NUMBER OF SEQ ID NOS: 65  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO: 52  
 ; LENGTH: 9  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Synthesized peptide

Query Match 100.0%; Score 41; DB 3; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLLQETELV 9  
 Db 1 RLLQETELV 9

RESULT 5  
 US-10-001-546-26  
 ; Sequence 26, Application US/10001546  
 ; Publication No. US2003027766A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: IOANNIDES, CONSTANTIN G.  
 ; APPLICANT: FISK, BRYAN A.  
 ; APPLICANT: IOANNIDES, MARIA G.  
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STIMULATING  
 ; T-LYMPHOCYTES  
 ; FILE REFERENCE: UTSC:390USC2  
 ; CURRENT APPLICATION NUMBER: US/10/001,546  
 ; CURRENT FILING DATE: 2001-03-31  
 ; PRIOR APPLICATION NUMBER: 08/403,459

PRIOR FILING DATE: 1995-03-14  
 NUMBER OF SEQ ID NOS: 68  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO: 26  
 LENGTH: 9  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 OTHER INFORMATION: Peptide  
 US-10-001-546-26

Query Match 100.0%; Score 41; DB 4; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
 Matches 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 RLLQETELV 9  
 Db 1 RLLQETELV 9

RESULT 6  
 US-10-001-013-40  
 Sequence 40, Application US/10080013  
 Publication No. US20030077248A1  
 GENERAL INFORMATION:  
 APPLICANT: Moriarty, Ann  
 APPLICANT: Leturcq, Didier  
 APPLICANT: Degraw, Juli  
 APPLICANT: Heiskala, Maria  
 APPLICANT: Peterson, Per  
 APPLICANT: Jackson, Michael  
 TITLE OF INVENTION: A CELL THERAPY METHOD FOR THE TREATMENT OF TUMORS  
 FILE REFERENCE: ORT-1557  
 CURRENT APPLICATION NUMBER: US/10/080,013  
 CURRENT FILING DATE: 2002-02-19  
 NUMBER OF SEQ ID NOS: 42  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO: 40  
 LENGTH: 9  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-080-013-40

Query Match 100.0%; Score 41; DB 4; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
 Matches 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 RLLQETELV 9  
 Db 1 RLLQETELV 9

RESULT 7  
 US-10-080-013-41  
 Sequence 41, Application US/10080013  
 Publication No. US20030077248A1  
 GENERAL INFORMATION:  
 APPLICANT: Moriarty, Ann  
 APPLICANT: Leturcq, Didier  
 APPLICANT: Degraw, Juli  
 APPLICANT: Heiskala, Maria  
 APPLICANT: Peterson, Per  
 APPLICANT: Jackson, Michael  
 TITLE OF INVENTION: A CELL THERAPY METHOD FOR THE TREATMENT OF TUMORS  
 FILE REFERENCE: ORT-1557  
 CURRENT APPLICATION NUMBER: US/10/080,013  
 CURRENT FILING DATE: 2002-02-19  
 NUMBER OF SEQ ID NOS: 42  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO: 41  
 LENGTH: 9  
 TYPE: PRT

; ORGANISM: Homo sapiens  
 US-10-080-013-41  
 Query Match 100.0%; Score 41; DB 4; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
 Matches 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 RLLQETELV 9  
 Db 1 RLLQETELV 9

RESULT 8  
 US-10-245-871-608  
 Sequence 608, Application US/10245871  
 Publication No. US2003023559A1  
 GENERAL INFORMATION:  
 APPLICANT: HUMPHREYS, ROBERT  
 APPLICANT: XU, MINZHEN  
 TITLE OF INVENTION: II-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES  
 FILE REFERENCE: REH-2013  
 CURRENT APPLICATION NUMBER: US/10/245,871  
 CURRENT FILING DATE: 2003-01-09  
 PRIOR APPLICATION NUMBER: 10/197,000  
 PRIOR FILING DATE: 2002-07-17  
 PRIOR APPLICATION NUMBER: 09/396,813  
 PRIOR FILING DATE: 1999-09-14  
 NUMBER OF SEQ ID NOS: 905  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO: 608  
 LENGTH: 9  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-245-871-608

Query Match 100.0%; Score 41; DB 4; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
 Matches 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 RLLQETELV 9  
 Db 1 RLLQETELV 9

RESULT 9  
 US-10-245-871-614  
 Sequence 614, Application US/10245871  
 Publication No. US2003023559A1  
 GENERAL INFORMATION:  
 APPLICANT: HUMPHREYS, ROBERT  
 APPLICANT: XU, MINZHEN  
 TITLE OF INVENTION: II-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES  
 FILE REFERENCE: REH-2013  
 CURRENT APPLICATION NUMBER: US/10/245,871  
 CURRENT FILING DATE: 2003-01-09  
 PRIOR APPLICATION NUMBER: 10/197,000  
 PRIOR FILING DATE: 2002-07-17  
 PRIOR APPLICATION NUMBER: 09/396,813  
 PRIOR FILING DATE: 1999-09-14  
 NUMBER OF SEQ ID NOS: 905  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO: 614  
 LENGTH: 9  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-245-871-614

Query Match 100.0%; Score 41; DB 4; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
 Matches 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 RLLQETELV 9

Db 1 RLLQETELV 9

RESULT 10  
US-10-149-138-671  
Sequence 671, Application US/10149138  
Publication No. US20040018971A1  
GENERAL INFORMATION:  
APPLICANT: Fikes, John  
APPLICANT: Sette, Alessandro  
APPLICANT: Sidney, John  
APPLICANT: Southwood, Scott  
APPLICANT: Cheanut, Robert  
APPLICANT: Celis, Esteban  
APPLICANT: Keogh, Elissa  
TITLE OF INVENTION: Inducing Cellular Immune Responses to HER2/neu Using Peptide and Nucleic Acid Compositions  
FILE REFERENCE: 2160\_0140001  
CURRENT APPLICATION NUMBER: US/10/149,138  
PRIORITY APPLICATION NUMBER: PCT/US00/33591  
CURRENT FILING DATE: 2002-06-10  
PRIOR FILING DATE: 2000-12-11  
PRIOR APPLICATION NUMBER: US 09/458,299  
PRIOR FILING DATE: 1999-12-11  
NUMBER OF SEQ ID NOS: 4641  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO: 671  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Artificially Synthesized Peptide  
US-10-149-138-671

Query Match 100.0%; Score 41; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLLQETELV 9  
Db 1 RLLQETELV 9

RESULT 11  
US-10-149-138-2276  
Sequence 2276, Application US/10149138  
Publication No. US20040018971A1  
GENERAL INFORMATION:  
APPLICANT: Fikes, John  
APPLICANT: Sette, Alessandro  
APPLICANT: Sidney, John  
APPLICANT: Southwood, Scott  
APPLICANT: Cheanut, Robert  
APPLICANT: Celis, Esteban  
APPLICANT: Keogh, Elissa  
TITLE OF INVENTION: Inducing Cellular Immune Responses to HER2/neu Using Peptide and Nucleic Acid Compositions  
FILE REFERENCE: 2160\_0140001  
CURRENT APPLICATION NUMBER: US/10/149,138  
PRIORITY APPLICATION NUMBER: PCT/US00/33591  
CURRENT FILING DATE: 2002-06-10  
PRIOR FILING DATE: 2000-12-11  
PRIOR APPLICATION NUMBER: US 09/458,299  
NUMBER OF SEQ ID NOS: 4641  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO: 2276  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Artificially Synthesized Peptide  
US-10-149-138-2276

Query Match 100.0%; Score 41; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLLQETELV 9  
Db 1 RLLQETELV 9

RESULT 12  
US-10-149-138-4420  
Sequence 4420, Application US/10149138  
Publication No. US20040018971A1  
GENERAL INFORMATION:  
APPLICANT: Fikes, John  
APPLICANT: Sette, Alessandro  
APPLICANT: Sidney, John  
APPLICANT: Southwood, Scott  
APPLICANT: Cheanut, Robert  
APPLICANT: Celis, Esteban  
APPLICANT: Keogh, Elissa  
TITLE OF INVENTION: Inducing Cellular Immune Responses to HER2/neu Using Peptide and Nucleic Acid Compositions  
FILE REFERENCE: 2060\_0140001  
CURRENT APPLICATION NUMBER: US/10/149,138  
CURRENT FILING DATE: 2002-06-10  
PRIOR APPLICATION NUMBER: PCT/US00/33591  
PRIOR FILING DATE: 2000-12-11  
PRIOR APPLICATION NUMBER: US 09/458,299  
PRIOR FILING DATE: 1999-12-11  
NUMBER OF SEQ ID NOS: 4641  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO: 4420  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Artificial Peptide  
US-10-149-138-4420

Query Match 100.0%; Score 41; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLLQETELV 9  
Db 1 RLLQETELV 9

RESULT 13  
US-10-447-161-88  
Sequence 88, Application US/10447161  
Publication No. US2004023314A1  
GENERAL INFORMATION:  
APPLICANT: Wang, Rong-fu  
TITLE OF INVENTION: Mutant Fibronectin and Tumor Metastasis  
FILE REFERENCE: HO-P02484US1  
CURRENT APPLICATION NUMBER: US/10/447,161  
CURRENT FILING DATE: 2003-05-28  
PRIOR APPLICATION NUMBER: 60/383,530  
PRIOR FILING DATE: 2002-05-28  
NUMBER OF SEQ ID NOS: 148  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO: 88  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic Peptide  
US-10-447-161-88

Query Match 100.0%; Score 41; DB 4; Length 9;

Best Local Similarity 100.0%; Pred. No. 1.7e+06; Mismatches 0; Indels 0; Gaps 0; Job time : 165 secs

Qy 1 RLLQETELV 9  
Db 1 RLLQETELV 9

## RESULT 14

US-10-253-286-608  
Sequence 608, Application US/102532886  
Publication No. US2004005881A1  
GENERAL INFORMATION:  
APPLICANT: HUMPHREYS, ROBERT  
TITLE OF INVENTION: II-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES  
FILE REFERENCE: REH-2015  
CURRENT APPLICATION NUMBER: US/10/253,286  
PRIORITY NUMBER: 10/197,000  
PRIOR FILING DATE: 2002-07-17  
PRIOR APPLICATION NUMBER: 09/396,813  
PRIOR FILING DATE: 1999-09-14  
NUMBER OF SEQ ID NOS: 905  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 608  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-253-286-608

Query Match 100.0%; Score 41; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06; Mismatches 0; Indels 0; Gaps 0;  
Matches 9; Conservative 0; Qy 1 RLLQETELV 9  
Db 1 RLLQETELV 9

## RESULT 15

US-10-253-286-614  
Sequence 614, Application US/102532886  
Publication No. US2004005881A1  
GENERAL INFORMATION:  
APPLICANT: HUMPHREYS, ROBERT  
TITLE OF INVENTION: II-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES  
FILE REFERENCE: REH-2015  
CURRENT APPLICATION NUMBER: US/10/253,286  
PRIORITY NUMBER: 10/197,000  
PRIOR FILING DATE: 2002-07-17  
PRIOR APPLICATION NUMBER: 09/396,813  
PRIOR FILING DATE: 1999-09-14  
NUMBER OF SEQ ID NOS: 905  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 614  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-253-286-614

Query Match 100.0%; Score 41; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06; Mismatches 0; Indels 0; Gaps 0;  
Matches 9; Conservative 0; Qy 1 RLLQETELV 9  
Db 1 RLLQETELV 9

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## OM protein - protein search, using sw model

Run on: March 1, 2006, 02:51:02 ; Search time 47 Seconds  
 (without alignments)  
 15.832 Million cell updates/sec

Title: US-09-583-200f-22  
 Perfect score: 41  
 Sequence: 1 RLUQETLV 9

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : Issued\_Patents\_AA:  
 1: /cgn2\_6/ptodata/1/iaa/5 COMB .pep: \*  
 2: /cgn2\_6/ptodata/1/iaa/6 \_COMB .pep: \*  
 3: /cgn2\_6/ptodata/1/iaa/H \_COMB .pep: \*  
 4: /cgn2\_6/ptodata/1/iaa/PCTUS COMB .pep: \*  
 5: /cgn2\_6/ptodata/1/iaa/RE COMB .pep: \*  
 6: /cgn2\_6/ptodata/1/iaa/backtles1.pep: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	41	100.0	9	1	US-08-467-083-6	Sequence 6, Appli
2	41	100.0	9	1	US-08-414-417B-6	Sequence 6, Appli
3	41	100.0	9	1	US-08-466-349A-6	Sequence 6, Appli
4	41	100.0	9	1	US-08-458-545B-6	Sequence 6, Appli
5	41	100.0	9	2	US-08-466-680B-6	Sequence 6, Appli
6	41	100.0	9	2	US-08-403-459-26	Sequence 26, Appli
7	41	100.0	9	2	US-09-543-608A-7	Sequence 7, Appli
8	41	100.0	9	2	US-09-354-533-6	Sequence 6, Appli
9	41	100.0	15	1	US-08-467-083-40	Sequence 40, Appli
10	41	100.0	15	1	US-08-414-417B-40	Sequence 40, Appli
11	41	100.0	15	1	US-08-456-349A-40	Sequence 40, Appli
12	41	100.0	15	1	US-08-468-545B-40	Sequence 40, Appli
13	41	100.0	15	2	US-08-456-680B-40	Sequence 40, Appli
14	41	100.0	15	2	US-09-354-533-40	Sequence 40, Appli
15	41	100.0	16	1	US-08-467-083-63	Sequence 63, Appli
16	41	100.0	16	1	US-08-414-417B-63	Sequence 63, Appli
17	41	100.0	16	1	US-08-456-349A-63	Sequence 63, Appli
18	41	100.0	16	1	US-08-468-545B-63	Sequence 63, Appli
19	41	100.0	16	2	US-08-456-680B-63	Sequence 63, Appli
20	41	100.0	16	2	US-09-354-533-63	Sequence 63, Appli
21	41	100.0	580	1	US-08-414-417B-69	Sequence 69, Appli
22	41	100.0	580	1	US-08-456-349A-69	Sequence 69, Appli
23	41	100.0	580	1	US-08-466-545B-69	Sequence 69, Appli
24	41	100.0	580	2	US-08-466-680B-69	Sequence 69, Appli
25	41	100.0	580	2	US-09-534-533-69	Sequence 69, Appli
26	41	100.0	1255	1	US-08-467-083-68	Sequence 68, Appli
27	41	100.0	1255	1	US-08-414-417B-68	Sequence 68, Appli

RESULT 1  
 US-08-467-083-6  
 ; Sequence 6, Application US/08467083  
 ; Patent No. 5726023

GENERAL INFORMATION:

APPLICANT: Cheever, Martin A.  
 APPLICANT: Dasis, Mary L.  
 TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/NEU PROTEIN FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE HER-2/NEU ONCOGENE IS ASSOCIATED

NUMBER OF SEQUENCES: 68

CORRESPONDENCE ADDRESS:

ADDRESSEE: Seed and Berry  
 STREET: 6300 Columbia Center, 701 Fifth Avenue  
 CITY: Seattle  
 STATE: Washington  
 COUNTRY: US  
 ZIP: 98104-7092

COMPUTER READABLE FORM:

COMPUTER: IBM PC Compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/467, 083  
 FILING DATE: 06-JUN-1995  
 CLASSIFICATION: 424  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/414, 417  
 FILING DATE: 06-JUN-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Sharkey, Richard G.  
 REGISTRATION NUMBER: 32, 629  
 REFERENCE/DOCKET NUMBER: 920010.448C2  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (206) 622-4900  
 TELEFAX: (206) 622-6031  
 TELEX: 3723336 SBE DANBERRY  
 INFORMATION FOR SEQ ID NO: 6:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 9 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 US-08-467-083-6

Query Match 100.0%; Score 41; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLLQETLV 9

Qy

DD 1 RLLQETELV 9

RESULT 2  
US-08-414-417B-6  
Sequence 6, Application US/08414417B  
Patent No. 5801005  
GENERAL INFORMATION:  
APPLICANT: Cheever, Martin A.  
APPLICANT: Disis, Mary L.  
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN  
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE  
TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED  
NUMBER OF SEQUENCES: 69  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/414,417B  
FILING DATE: 31-MAR-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Sharkey, Richard G.  
REGISTRATION NUMBER: 32,629  
REFERENCE/DOCKET NUMBER: 920010.448C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-0311  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-414-417B-6

Query Match 100.0%; Score 41; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLLQETELV 9  
Db 1 RLLQETELV 9

RESULT 4  
US-08-468-545B-6  
Sequence 6, Application US/08468545B  
Patent No. 5816712  
GENERAL INFORMATION:  
APPLICANT: Cheever, Martin A.  
APPLICANT: Disis, Mary L.  
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN  
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE  
TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED  
NUMBER OF SEQUENCES: 69  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/468,545B  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Sharkey, Richard G.  
REGISTRATION NUMBER: 32,629  
REFERENCE/DOCKET NUMBER: 920010.448C5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-468-545B-6

Query Match 100.0%; Score 41; DB 1; Length 9;

Qy 1 RLLQETELV 9  
Db 1 RLLQETELV 9

RESULT 3  
US-08-486-349A-6  
Sequence 6, Application US/08486348A  
Patent No. 5846538  
GENERAL INFORMATION:  
APPLICANT: Cheever, Martin A.  
APPLICANT: Disis, Mary L.  
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN  
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE  
TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED  
NUMBER OF SEQUENCES: 69  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:

Best Local Similarity 100.0%; Pred. No. 4.6e+05; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLLQETELV 9  
Db 1 RLLQETELV 9

RESULT 5  
US-08-466-680B-6  
Sequence 6, Application US/08466680B  
Patent No. 6075122  
GENERAL INFORMATION:  
APPLICANT: Cheever, Martin A.  
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN  
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED  
NUMBER OF SEQUENCES: 69  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092

COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/4666,680B  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Sharkey, Richard G.  
REGISTRATION NUMBER: 32,629  
REFERENCE/DOCKET NUMBER: 920010.448C4  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
TOPOLOGY: linear

US-08-466-680B-6  
Query Match Best Local Similarity 100.0%; Pred. No. 4.6e+05; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLLQETELV 9  
Db 1 RLLQETELV 9

RESULT 6  
US-08-403-459-26  
Sequence 26, Application US/08403459  
Patent No. 6514942  
GENERAL INFORMATION:  
APPLICANT: Ioannides, Constantine G.  
APPLICANT: Fisk, Bryan A.  
APPLICANT: Ioannides, Maria G.  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STIMULATING NUMBER OF SEQUENCES: 68  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston

STATE: Texas  
COUNTRY: United States of America  
ZIP: 77110  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/403,459  
FILING DATE: Concurrently Herewith  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Kilchell, Barbara S.  
REGISTRATION NUMBER: 33,928  
REFERENCE DOCKET NUMBER: UTSC:390/KIT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (512) 418-3000  
TELEFAX: (713) 789-2679  
TELEX: 79-0924  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-403-459-26  
Query Match Best Local Similarity 100.0%; Pred. No. 4.6e+05; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLLQETELV 9  
Db 1 RLLQETELV 9

RESULT 7  
US-09-543-608A-7  
Sequence 7, Application US/09543608A  
Patent No. 660510  
GENERAL INFORMATION:  
APPLICANT: Elkes, John D.  
APPLICANT: Sette, Alessandro  
APPLICANT: Sidney, John  
APPLICANT: Southwood, Scott  
APPLICANT: Celis, Esteban  
APPLICANT: Keogh, Ellesa A.  
APPLICANT: Chernet, Robert  
APPLICANT: Epimmune Inc.  
TITLE OF INVENTION: HLA Class I A2 Tumor Associated Antigen  
TITLE OF INVENTION: Peptides and Vaccine Compositions  
FILE REFERENCE: 018623-01571US  
CURRENT FILING DATE: 2002-04-05  
NUMBER OF SEQ ID NOS: 52  
SOFTWARE: FastSEQ for Windows Version 3.0  
SEQ ID NO: 7  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: HER2/neu.689

US-09-543-608A-7  
Query Match Best Local Similarity 100.0%; Pred. No. 4.6e+05; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLLQETELV 9  
Db 1 RLLQETELV 9

RESULT 8  
US-09-354-533-6  
Sequence 6, Application US/09354533  
Patent No. 6664310  
GENERAL INFORMATION:  
APPLICANT: Cheever, Martin A.  
DISIS, Mary L.  
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE HER-2/neu ONCOGENE IS ASSOCIATED

NUMBER OF SEQUENCES: 69  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/354,533  
FILING DATE: 15-Jul-1999  
CLASSIFICATION: <Unknown>  
NAME: Sharkey, Richard G.  
REGISTRATION NUMBER: 32,629  
REFERENCE/DOCKET NUMBER: 920010.448C9  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 682-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-09-354-533-6

Query Match 100.0%; Score 41; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 4.0e+05; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLLQETEV 9  
Db 6 RLLQETEV 14

RESULT 10  
US-08-414-417B-40  
Sequence 40, Application US/08414417B  
Patent No. 5801005  
GENERAL INFORMATION:  
APPLICANT: Cheever, Martin A.  
DISIS, Mary L.  
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE HER-2/neu ONCOGENE IS ASSOCIATED  
NUMBER OF SEQUENCES: 69  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
COUNTRY: Washington  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/414,417B  
FILING DATE: 31-Mar-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Sharkey, Richard G.  
REGISTRATION NUMBER: 32,629  
REFERENCE/DOCKET NUMBER: 920010.448C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 682-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 40:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: linear

RESULT 9  
US-08-467-083-40  
Sequence 40, Application US/08467083  
Patent No. 5726023  
GENERAL INFORMATION:  
APPLICANT: Cheever, Martin A.  
DISIS, Mary L.  
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/NEU PROTEIN FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE HER-2/NEU ONCOGENE IS ASSOCIATED  
NUMBER OF SEQUENCES: 68  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

US-08-414-417B-40  
 Query Match 100.0%; Score 41; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 0.087; Indels 0; Gaps 0;  
 Matches 9; Conservative 0; Mismatches 0;  
 Qy 1 RLLQETELV 9  
 Db 6 RLLQETELV 14

RESULT 11  
 US-08-486-348A-40  
 ; Sequence 40, Application US/08486348A  
 ; Patent No. 5846338  
 GENERAL INFORMATION:  
 ; APPLICANT: Cheever, Martin A.  
 ; APPLICANT: Disis, Mary L.  
 ; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN  
 ; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE  
 ; TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED  
 ; NUMBER OF SEQUENCES: 69  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Seed and Berry LLP  
 ; STREET: 6300 Columbia Center, 701 Fifth Avenue  
 ; CITY: Seattle  
 ; STATE: Washington  
 ; COUNTRY: US  
 ; ZIP: 98104-7092  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/486, 545B  
 ; FILING DATE: 06-JUN-1995  
 ; CLASSIFICATION: 424  
 ATTORNEY/AGENT INFORMATION:  
 ; NAME: Sharkey, Richard G.  
 ; REGISTRATION NUMBER: 32,629  
 ; REFERENCE/DOCKET NUMBER: 920010.448C5  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (206) 622-4900  
 ; TELEFAX: (206) 682-6031  
 ; INFORMATION FOR SEQ ID NO: 40:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 15 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; US-08-468-545B-40

Query Match 100.0%; Score 41; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 0.087; Indels 0; Gaps 0;  
 Matches 9; Conservative 0; Mismatches 0;

Qy 1 RLLQETELV 9  
 Db 6 RLLQETELV 14

RESULT 12  
 US-08-486-545B-40  
 ; Sequence 40, Application US/08486545B  
 ; Patent No. 5876712  
 GENERAL INFORMATION:  
 ; APPLICANT: Cheever, Martin A.  
 ; APPLICANT: Disis, Mary L.  
 ; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN  
 ; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE  
 ; TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED  
 ; NUMBER OF SEQUENCES: 69  
 ; CORRESPONDENCE ADDRESS:

ADDRESSEE: Seed and Berry LLP  
 ; STREET: 6300 Columbia Center, 701 Fifth Avenue  
 ; CITY: Seattle  
 ; STATE: Washington  
 ; COUNTRY: US  
 ; ZIP: 98104-7092  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/468, 545B  
 ; FILING DATE: 06-JUN-1995  
 ; CLASSIFICATION: 424  
 ATTORNEY/AGENT INFORMATION:  
 ; NAME: Sharkey, Richard G.  
 ; REGISTRATION NUMBER: 32,629  
 ; REFERENCE/DOCKET NUMBER: 920010.448C5  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (206) 622-4900  
 ; TELEFAX: (206) 682-6031  
 ; INFORMATION FOR SEQ ID NO: 40:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 15 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; US-08-468-545B-40

Query Match 100.0%; Score 41; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 0.087; Indels 0; Gaps 0;  
 Matches 9; Conservative 0; Mismatches 0;

Qy 1 RLLQETELV 9  
 Db 6 RLLQETELV 14

RESULT 13  
 US-08-466-660B-40  
 ; Sequence 40, Application US/084666680B  
 ; Patent No. 607512  
 GENERAL INFORMATION:  
 ; APPLICANT: Cheever, Martin A.  
 ; APPLICANT: Disis, Mary L.  
 ; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN  
 ; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE  
 ; TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED  
 ; NUMBER OF SEQUENCES: 69  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Seed and Berry LLP  
 ; STREET: 6300 Columbia Center, 701 Fifth Avenue  
 ; CITY: Seattle  
 ; STATE: Washington  
 ; COUNTRY: US  
 ; ZIP: 98104-7092  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/466, 660B  
 ; FILING DATE: 06-JUN-1995  
 ; CLASSIFICATION: 424  
 ATTORNEY/AGENT INFORMATION:  
 ; NAME: Sharkey, Richard G.  
 ; REGISTRATION NUMBER: 32,629  
 ; REFERENCE/DOCKET NUMBER: 920010.448C4  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (206) 622-4900  
 ; TELEFAX: (206) 682-6031  
 ; INFORMATION FOR SEQ ID NO: 40:

SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
US-08-4665-680B-40

Query Match      Best Local Similarity      Score      DB 2;      Length 15;  
Matches      9;      Conservative      0;      Mismatches      0;      Indels      0;      Gaps      0;

QY      1 RLLQETELV 9  
Db      6 RLLQETELV 14

RESULT 14  
US-09-354-533-40  
Sequence 40, Application US/09354533  
Patent No. 6664310

GENERAL INFORMATION:  
APPLICANT: Cheever, Martin A.  
DIS, Mary L.

TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE HER-2/neu ONCOGENE IS ASSOCIATED

NUMBER OF SEQUENCES: 69

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US

ZIP: 98104-7092

COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/467,083  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 424  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/414,417  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Sharkey, Richard G.  
REGISTRATION NUMBER: 32,629  
REFERENCE/DOCKET NUMBER: 920010.448C2

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
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TELEX: 372326 SEEDANBERRY

INFORMATION FOR SEQ ID NO: 63:

SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear

US-08-467-083-63

Query Match      Best Local Similarity      Score      DB 1;      Length 16;  
Matches      9;      Conservative      0;      Mismatches      0;      Indels      0;      Gaps      0;

Qy      1 RLLQETELV 9  
Db      2 RLLQETELV 10

Search completed: March 1, 2006, 02:52:24  
Job time : 48 secs

RESULT 15  
US-08-467-083-63  
Sequence 63, Application US/08467083  
Patent No. 572603  
GENERAL INFORMATION:  
APPLICANT: Cheever, Martin A.  
APPLICANT: Disis, Mary L.

Query Match      Best Local Similarity      Score      DB 2;      Length 15;  
Matches      9;      Conservative      0;      Mismatches      0;      Indels      0;      Gaps      0;

QY      1 RLLQETELV 9  
Db      6 RLLQETELV 14

US-09-354-533-40

Query Match      Best Local Similarity      Score      DB 2;      Length 15;  
Matches      9;      Conservative      0;      Mismatches      0;      Indels      0;      Gaps      0;

QY      1 RLLQETELV 9  
Db      6 RLLQETELV 14